

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 28, 2004, 08:56:55 ; Search time 59.4242 Seconds
(without alignments)
2462.961 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALARALLPLLAQWLLRA.....RPRDPEVVNDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2687	100.0	518	2	AAW61362	Aaw61362 Aspartic
2	2687	100.0	518	2	AAy13799	Aay13799 Human asp
3	2687	100.0	518	2	AAy22239	Aay22239 Human CSP
4	2687	100.0	518	2	AAy41714	Aay41714 Human PRO
5	2687	100.0	518	3	AAy88424	Aay88424 Human asp
6	2687	100.0	518	3	AAB44270	Aab44270 Human PRO
7	2687	100.0	518	4	AAU07201	Aau07201 Human asp
8	2687	100.0	518	4	AAE10628	Aae10628 Human asp
9	2687	100.0	518	4	AAE10656	Aae10656 Human-Asp

10	2687	100.0	518	4	AAE06858	Aae06858	Human	asp
11	2687	100.0	518	4	AAE02608	Aae02608	Human	Asp
12	2687	100.0	518	4	AAE02580	Aae02580	Human	asp
13	2687	100.0	518	4	AAU29059	Aau29059	Human	PRO
14	2687	100.0	518	4	AAU06602	Aau06602	Human	Asp
15	2687	100.0	518	5	ABB06531	Abb06531	Human	asp
16	2687	100.0	518	5	ABB78589	Abb78589	Human	Asp
17	2687	100.0	518	5	ABB78617	Abb78617	Human	Asp
18	2687	100.0	518	5	ABB07453	Abb07453	Human	BAC
19	2687	100.0	518	6	ABU58435	Abu58435	Human	PRO
20	2687	100.0	518	6	ABU87983	Abu87983	Novel	hum
21	2687	100.0	518	6	ABU84298	Abu84298	Human	sec
22	2687	100.0	518	6	ABR66172	Abr66172	Human	sec
23	2687	100.0	518	6	ABR65562	Abr65562	Human	sec
24	2687	100.0	518	6	ABU99502	Abu99502	Human	sec
25	2687	100.0	518	6	ABU82741	Abu82741	Human	PRO
26	2687	100.0	518	6	ABU89862	Abu89862	Novel	hum
27	2687	100.0	518	6	ABR68111	Abr68111	Human	sec
28	2687	100.0	518	6	ABU96164	Abu96164	Novel	hum
29	2687	100.0	518	6	ABU92595	Abu92595	Human	sec
30	2687	100.0	518	6	ABO08672	Abo08672	Human	sec
31	2687	100.0	518	6	ABO02724	Abo02724	Human	sec
32	2687	100.0	518	6	ABR74878	Abr74878	Human	sec
33	2687	100.0	518	6	ABR94640	Abr94640	Human	sec
34	2687	100.0	518	6	ABO25216	Abo25216	Novel	hum
35	2687	100.0	518	6	ABU85613	Abu85613	Human	PRO
36	2687	100.0	518	6	ABU98773	Abu98773	Novel	hum
37	2687	100.0	518	6	ABU97988	Abu97988	Novel	hum
38	2687	100.0	518	6	ABU91694	Abu91694	Novel	hum
39	2687	100.0	518	6	ABU72222	Abu72222	Novel	hum
40	2687	100.0	518	6	ABU89387	Abu89387	Human	PRO
41	2687	100.0	518	6	ABU86228	Abu86228	Human	sec
42	2687	100.0	518	6	ABU67441	Abu67441	Human	sec
43	2687	100.0	518	6	ABU80469	Abu80469	Human	PRO
44	2687	100.0	518	6	ABR99387	Abr99387	Human	sec
45	2687	100.0	518	6	ABR98777	Abr98777	Human	sec

ALIGNMENTS

RESULT 1

AAW61362

ID AAW61362 standard; protein; 518 AA.

XX

AC AAW61362;

XX

DT 25-MAR-2003 (revised)

DT 25-SEP-1998 (first entry)

XX

DE Aspartic proteinase ASP1.

XX

KW ASP1; Aspartic proteinase; Alzheimer's disease; cancer; melanoma.

XX

OS Homo sapiens.

XX

PN EP848062-A2.

XX
PD 17-JUN-1998.
XX
PF 01-DEC-1997; 97EP-00309648.
XX
PR 14-DEC-1996; 96GB-00026022.
PR 06-OCT-1997; 97US-00999723.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Powell DJ, Southan C, Chapman CG, Evans JR;
XX
DR WPI; 1998-314477/28.
DR N-PSDB; AAV27962.
XX
PT New isolated polynucleotide encodes Aspartic protease polypeptide - used
PT to diagnosis, treat and vaccinate against Alzheimer's disease, cancer and
PT melanoma.
XX
PS Claim 11; Page 7; 19pp; English.
XX
CC The human ASP1 protein is structurally related to other proteins of the
CC Aspartic proteinase family. ASP 1 polypeptides and polynucleotides can be
CC used to diagnosis, treat and vaccinate against Alzheimer's disease,
CC cancer and melanoma. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 2; Length 518;
Best Local Similarity 100.0%; Pred. No. 8.6e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP	60
Qy	61	ALALEPALASPAGAAFLAMVDNLQGD	120
Db	61	ALALEPALASPAGAAFLAMVDNLQGD	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGF	180
Db	121	TPHSYIDTYFDTERSSTYRSKGF	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Qy	241	GSQTNGGSLVLGGIEPSLYKGDIWYTPIKEEWWYQIEILKLEIGGQSLNLD	300
Db	241	GSQTNGGSLVLGGIEPSLYKGDIWYTPIKEEWWYQIEILKLEIGGQSLNLD	300
Qy	301	IVDSGT'TLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ	360
Db	301	IVDSGT'TLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ	360

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QY      361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
          |||
Db      361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

QY      421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
          |||
Db      421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

QY      481 AILLVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518
          |||
Db      481 AILLVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518

```

RESULT 2

AAY13799

ID AAY13799 standard; protein; 518 AA.

XX

AC AAY13799;

XX

DT 21-SEP-1999 (first entry)

XX

DE Human aspartyl protease, CSP56.

XX

KW CSP56; human; aspartyl protease; diagnosis; neoplasia; tumour;

KW breast tumour; colon tumour.

XX

OS Homo sapiens.

XX

PN WO9933963-A1.

XX

PD 08-JUL-1999.

XX

PF 14-DEC-1998; 98WO-US026547.

XX

PR 31-DEC-1997; 97US-0070112P.

XX

PA (CHIR) CHIRON CORP.

XX

PI Giese KW, Xin H;

XX

DR WPI; 1999-430240/36.

DR N-PSDB; AAX89297.

XX

PT Human CSP56 protein for diagnosis of neoplasia.

XX

PS Claim 2; Fig 2A; 5lpp; English.

XX

CC This represents a human CSP56 protein, a novel aspartyl protease. The
 CC CSP56 protein can be used in methods for diagnosing neoplasia, for
 CC determining the metastatic potential of a tumour, and for screening test
 CC compounds for the ability to suppress the metastatic potential of a
 CC tumour. The tumours are preferably from breast or colon

XX

SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 2; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.6e-231;

Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGL	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGL	60
Qy	61	ALALEPALASPAGAAFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAAFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGVGEDLVITPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFGVGEDLVITPKGFNTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Qy	241	GGGTNGGSLVLGGIEPSLYKGGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Db	241	GGGTNGGSLVLGGIEPSLYKGGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Qy	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Db	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Qy	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480
Db	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480
Qy	481	AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK	518
Db	481	AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK	518

RESULT 3

AAAY22239

ID AAY22239 standard; protein; 518 AA.

XX

AC AAY22239;

XX

DT 20-SEP-1999 (first entry)

XX

DE Human CSP56, aspartyl-type protease, protein sequence.

XX

KW Metastatic marker protein; human; cancer metastasis; breast cancer;
 KW colon cancer; diagnosis; therapy; tumour; metastatic potential; CSP56;
 KW aspartyl-type protease.

XX

OS Homo sapiens.

XX

PN WO9934004-A2.

XX

PD 08-JUL-1999.
 XX
 PF 24-DEC-1998; 98WO-US027608.
 XX
 PR 31-DEC-1997; 97US-0070112P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Xin H, Giese K;
 XX
 DR WPI; 1999-430248/36.
 DR N-PSDB; AAX84708.
 XX
 PT New polynucleotides associated with cancer metastasis.
 XX
 PS Claim 4; Page 78-80; 80pp; English.
 XX
 CC This sequence represents a polypeptide of the invention, and is an
 CC aspartyl-type protease, designated CSP56. The polynucleotides (PNs) of
 CC the invention encode metastatic marker protein variants. The PNs and
 CC polypeptides can be used as markers for cancer metastasis. The products
 CC can be used for identifying metastatic tissue or metastatic potential of
 CC a tissue, e.g. breast or colon tissue. They can also be used for
 CC screening test compounds for the ability to suppress the metastatic
 CC potential of a tumour. The products can be used for developing products
 CC for the therapy of cancers, particularly breast or colon cancer
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 2; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.6e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGL	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGL	60
Qy	61	ALALEPALASPAGAAANFLAMVDNLQGDSSRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAAANFLAMVDNLQGDSSRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMQMCGAGLPVA	240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMQMCGAGLPVA	240
Qy	241	GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA	300
Db	241	GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360

Qy 361 YLRDENSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
 |||
 Db 361 YLRDENSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
 |||
 Db 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

Qy 481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
 |||
 Db 481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518

RESULT 4

AA41714

ID AA41714 standard; protein; 518 AA.

XX

AC AA41714;

XX

DT 07-DEC-1999 (first entry)

XX

DE Human PRO852 protein sequence.

XX

KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.

XX

OS Homo sapiens.

XX

PN WO9946281-A2.

XX

PD 16-SEP-1999.

XX

PF 08-MAR-1999; 99WO-US005028.

XX

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077641P.

PR 11-MAR-1998; 98US-0077649P.

PR 12-MAR-1998; 98US-0077791P.

PR 13-MAR-1998; 98US-0078004P.

PR 17-MAR-1998; 98US-00040220.

PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078910P.

PR 20-MAR-1998; 98US-0078936P.

PR 20-MAR-1998; 98US-0078939P.

PR 25-MAR-1998; 98US-0079294P.

PR 26-MAR-1998; 98US-0079656P.

PR 27-MAR-1998; 98US-0079663P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079689P.

PR 27-MAR-1998; 98US-0079728P.

PR 27-MAR-1998; 98US-0079786P.

PR 30-MAR-1998; 98US-0079920P.

PR 30-MAR-1998; 98US-0079923P.

PR 31-MAR-1998; 98US-0080105P.

PR 31-MAR-1998; 98US-0080107P.

PR	31-MAR-1998;	98US-0080165P.
PR	31-MAR-1998;	98US-0080194P.
PR	01-APR-1998;	98US-0080327P.
PR	01-APR-1998;	98US-0080328P.
PR	01-APR-1998;	98US-0080333P.
PR	01-APR-1998;	98US-0080334P.
PR	08-APR-1998;	98US-0081049P.
PR	08-APR-1998;	98US-0081070P.
PR	08-APR-1998;	98US-0081071P.
PR	09-APR-1998;	98US-0081195P.
PR	09-APR-1998;	98US-0081203P.
PR	09-APR-1998;	98US-0081229P.
PR	15-APR-1998;	98US-0081817P.
PR	15-APR-1998;	98US-0081838P.
PR	15-APR-1998;	98US-0081952P.
PR	15-APR-1998;	98US-0081955P.
PR	21-APR-1998;	98US-0082568P.
PR	21-APR-1998;	98US-0082569P.
PR	22-APR-1998;	98US-0082700P.
PR	22-APR-1998;	98US-0082704P.
PR	22-APR-1998;	98US-0082804P.
PR	23-APR-1998;	98US-0082767P.
PR	23-APR-1998;	98US-0082796P.
PR	27-APR-1998;	98US-0083336P.
PR	28-APR-1998;	98US-0083322P.
PR	29-APR-1998;	98US-0083392P.
PR	29-APR-1998;	98US-0083495P.
PR	29-APR-1998;	98US-0083496P.
PR	29-APR-1998;	98US-0083499P.
PR	29-APR-1998;	98US-0083500P.
PR	29-APR-1998;	98US-0083545P.
PR	29-APR-1998;	98US-0083554P.
PR	29-APR-1998;	98US-0083558P.
PR	29-APR-1998;	98US-0083559P.
PR	30-APR-1998;	98US-0083742P.
PR	05-MAY-1998;	98US-0084366P.
PR	06-MAY-1998;	98US-0084414P.
PR	06-MAY-1998;	98US-0084441P.
PR	07-MAY-1998;	98US-0084598P.
PR	07-MAY-1998;	98US-0084600P.
PR	07-MAY-1998;	98US-0084627P.
PR	07-MAY-1998;	98US-0084637P.
PR	07-MAY-1998;	98US-0084639P.
PR	07-MAY-1998;	98US-0084640P.
PR	07-MAY-1998;	98US-0084643P.
PR	13-MAY-1998;	98US-0085323P.
PR	13-MAY-1998;	98US-0085338P.
PR	13-MAY-1998;	98US-0085339P.
PR	15-MAY-1998;	98US-0085573P.
PR	15-MAY-1998;	98US-0085579P.
PR	15-MAY-1998;	98US-0085580P.
PR	15-MAY-1998;	98US-0085582P.
PR	15-MAY-1998;	98US-0085689P.
PR	15-MAY-1998;	98US-0085697P.
PR	15-MAY-1998;	98US-0085700P.
PR	15-MAY-1998;	98US-0085704P.
PR	18-MAY-1998;	98US-0086023P.


```

Db      241  ||||| GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300
Qy      301  IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
Db      301  ||||| IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
Qy      361  YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
Db      361  ||||| YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
Qy      421  RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCG 480
Db      421  ||||| RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCG 480
Qy      481  AILLVLIVLLLLPFR CQRRPRDPEVVNDESSLVRHRWK 518
Db      481  ||||| AILLVLIVLLLLPFR CQRRPRDPEVVNDESSLVRHRWK 518

```

RESULT 5

AA Y88424

ID AAY88424 standard; protein; 518 AA.

XX

AC AAY88424;

XX

DT 03-AUG-2000 (first entry)

XX

DE Human aspartyl protease 1 (Asp1) amino acid sequence.

XX

KW Aspartyl protease; aspartase; amyloid precursor protein; APP; Asp 1;

KW Alzheimer's disease; beta secretase site.

XX

OS Homo sapiens.

XX

PN WO200017369-A2.

XX

PD 30-MAR-2000.

XX

PF 23-SEP-1999; 99WO-US020881.

XX

PR 24-SEP-1998; 98US-0101594P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2000-303209/26.

DR N-PSDB; AAA15661.

XX

PT New enzyme designated human aspartase useful in research into Alzheimer's

PT Disease is capable of cleaving amyloid protein precursor at the beta

PT secretase site to produce amyloid beta peptide.

XX

PS Claim 54; Fig 1; 183pp; English.

XX

CC This sequence represents the human aspartyl protease amino acid sequence.

CC The invention relates to a protease capable of cleaving the beta
CC secretase site of amyloid precursor protein (APP). The protease contains
CC a sequence encoding the amino acid sequence DTG and a sequence encoding
CC DSG or DTG separated by 100-300 amino acids. When mutated the APP gene
CC causes an autosomal dominant form of Alzheimer's disease. APP localises
CC to the cell surface membrane and have a single C-terminal transmembrane
CC domain. Proteolytic processing of APP produces the amyloid beta protein,
CC which is possibly very important in Alzheimer's disease. The invention
CC includes a nucleotide sequence encoding the protease, a vector containing
CC the nucleotide sequence, and a cell line comprising the vector. Methods
CC for screening for inhibitors of beta secretase activity are also given in
CC the invention. The human aspartase protein and nucleotide sequences and
CC the methods for identifying inhibitors of the protease, are useful in the
CC treatment of and research in to Alzheimer's disease

XX

SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 3; Length 518;
Best Local Similarity 100.0%; Pred. No. 8.6e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP	60
Qy	61	ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGENTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGENTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFSDSLVTQANIPNVFSMQMCGAGLPVA	240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFSDSLVTQANIPNVFSMQMCGAGLPVA	240
Qy	241	GSQTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Db	241	GSQTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Qy	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Db	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Qy	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480
Db	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480
Qy	481	AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK	518
Db	481	AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK	518

RESULT 6

AAB44270

ID AAB44270 standard; protein; 518 AA.

XX

AC AAB44270;

XX

DT 08-FEB-2001 (first entry)

XX

DE Human PRO852 (UNQ418) protein sequence SEQ ID NO:196.

XX

KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.

XX

OS Homo sapiens.

XX

PN WO200053756-A2.

XX

PD 14-SEP-2000.

XX

PF 18-FEB-2000; 2000WO-US004341.

XX

PR 08-MAR-1999; 99WO-US005028.

PR 12-MAR-1999; 99US-0123957P.

PR 29-MAR-1999; 99US-0126773P.

PR 21-APR-1999; 99US-0130232P.

PR 28-APR-1999; 99US-0131445P.

PR 14-MAY-1999; 99US-0134287P.

PR 23-JUN-1999; 99US-0141037P.

PR 26-JUL-1999; 99US-0145698P.

PR 29-OCT-1999; 99US-0162506P.

PR 30-NOV-1999; 99WO-US028313.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 30-DEC-1999; 99WO-US031243.

PR 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

XX

PA (GETH) GENENTECH INC.

XX

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;

PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL;

PI Stewart TA, Tumas D, Williams PM, Wood WI;

XX

DR WPI; 2000-611443/58.

DR N-PSDB; AAC78500.

XX

PT Novel PRO polypeptides and polynucleotides used in detection methods, to
PT target bioactive molecules to specific cells, and to modulate cellular
PT activities.

XX

PS Claim 12; Fig 73; 636pp; English.

XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence
 CC tag) sequences which encode secreted or transmembrane PRO polypeptides.
 CC The PRO polynucleotides and polypeptides have cytostatic activity. The
 CC polynucleotides and polypeptides can be used for detecting the presence
 CC of PRO polypeptides in samples, for linking bioactive molecules to cells
 CC and for modulating biological activities of cells, using the polypeptides
 CC for specific targeting. The polypeptide targeting can be used to kill the
 CC target cells, e.g. for the treatment of cancers. The polypeptide pairs
 CC provide specific targeting of bioactive molecules to cells. AAC78600 to
 CC AAC78987 represent PCR primers and probes used in the isolation of the
 CC PRO polynucleotide sequences

XX

SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 3; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.6e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGL	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGL	60
Qy	61	ALALEPALASPAGAAFLAMVDNLQDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAAFLAMVDNLQDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Qy	241	GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA	300
Db	241	GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Qy	361	YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Db	361	YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Qy	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480
Db	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480
Qy	481	AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK	518
Db	481	AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK	518

RESULT 7

AAU07201

ID AAU07201 standard; protein; 518 AA.

XX

AC AAU07201;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human aspartyl protease 1 (Asp-1).

XX

KW Human; aspartyl protease 1; Asp-1; nootropic; neuroprotective;

KW aspartyl protease 2; Asp2; amyloid protein precursor; APP;

KW beta-secretase; Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200149097-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000797.

XX

PR 09-MAY-2001; 2001WO-IB000797.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.

XX

PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

XX

DR WPI; 2001-502548/55.

DR N-PSDB; AAS11701.

XX

PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.

XX

PS Example 2; Fig 1; 185pp; English.

XX

CC The invention relates to a novel purified polypeptide comprising a
CC fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the
CC Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide
CC and the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. Also included is an isoform of amyloid protein precursor (APP)
CC comprising the amino acid sequence of a APP or its fragment containing an
CC APP cleavage site recognisable by a mammalian beta-secretase, and further
CC comprising two lysine residues at the carboxyl terminus of the amino acid
CC sequence of the mammalian APP or APP fragment. The polypeptides are used
CC for assaying for modulators of beta-secretase activity; identifying
CC agents that inhibit the APP processing activity of human Asp2 aspartyl
CC protease (Hu-Asp2); identifying agents that modulate the activity of Asp2
CC ; and for reducing cellular production of amyloid beta (Abeta) from APP.
CC Agents identified by the above methods are useful for treating
CC Alzheimer's disease; and for identifying modulators of amyloid-beta
CC (Abeta) peptide production, for use in designing therapeutics for the

CC treatment or prevention of Alzheimer's disease. Probes and primers
 CC derived from Asp nucleic acid sequences are useful for detecting Hu-Asp
 CC nucleic acids in in vitro assays and in Northern and Southern blots. The
 CC present sequence represents the amino acid sequence of human Asp-1
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 4; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.6e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPPTAERHADGL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPPTAERHADGL 60

Qy     61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180

Qy    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy    241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300

Qy    301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360

Qy    361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy    421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

Qy    481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
      ||||||||||||||||||||||||||||||||||||
Db    481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518

```

RESULT 8
 AAE10628
 ID AAE10628 standard; protein; 518 AA.
 XX
 AC AAE10628;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Human aspartyl protease 1 (hu-Asp1) protein.

XX
 KW Human; aspartyl protease 1; Aspl; amyloid precursor protein; APP;
 KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;
 KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective;
 KW chromosome 21.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .20
 FT /label= Signal_peptide
 FT Protein 21. .518
 FT /note= "Mature human aspartyl protease 1"
 FT Domain 469. .492
 FT /label= Transmembrane_domain
 XX
 PN GB2357767-A.
 XX
 PD 04-JUL-2001.
 XX
 PF 22-SEP-2000; 2000GB-00023315.
 XX
 PR 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2001-444208/48.
 DR N-PSDB; AAD17864.
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with amyloid
 PT precursor protein processing activity and alpha-secretase activity, for
 PT identifying modulators useful in treating Alzheimer's disease.
 XX
 PS Claim 36; Fig 1; 187pp; English.
 XX
 CC The patent discloses human aspartyl protease 1 (hu-Aspl) or modified Aspl
 CC proteins which lack transmembrane domain or amino terminal domain or
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid
 CC protein precursor (APP) processing activity. The proteins of the
 CC invention are useful for assaying hu-Aspl alpha-secretase activity, which
 CC in turn is useful for identifying modulators of hu-Aspl alpha-secretase
 CC activity, where modulators that increase hu-Aspl alpha-secretase activity
 CC are useful for treating Alzheimer's disease (AD) which causes progressive
 CC dementia with consequent formation of amyloid plaques, neurofibrillary
 CC tangles, gliosis and neuronal loss. Hu-Aspl protease substrate is useful
 CC for assaying hu-Aspl proteolytic activity, by contacting hu-Aspl protein
 CC with the substrate under acidic conditions and determining the level of
 CC hu-Aspl proteolytic activity. The present sequence is Aspl protein from
 CC human. Aspl gene is localised on chromosome 21
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 4; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.6e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPATPAERHADGL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPATPAERHADGL 60

Qy     61 ALALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ALALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180

Qy    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMQMCGAGLPVA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMQMCGAGLPVA 240

Qy    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300

Qy    301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360

Qy    361 YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy    421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

Qy    481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518

```

RESULT 9

AAE10656

ID AAE10656 standard; protein; 518 AA.

XX

AC AAE10656;

XX

DT 10-DEC-2001 (first entry)

XX

DE Human-Asp 1 protein lacking TM domain and containing (His)6 tag.

XX

KW Human; aspartyl protease 1; Asp1; amyloid precursor protein; APP;

KW Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;

KW amyloid plaque; neuronal loss; proteolytic; nootropic; neuroprotective.

XX

OS Homo sapiens.

OS Synthetic.
 XX
 PN GB2357767-A.
 XX
 PD 04-JUL-2001.
 XX
 PF 22-SEP-2000; 2000GB-00023315.
 XX
 PR 23-SEP-1999; 99US-00404133.
 PR 23-SEP-1999; 99US-0155493P.
 PR 23-SEP-1999; 99WO-US020881.
 PR 13-OCT-1999; 99US-00416901.
 PR 06-DEC-1999; 99US-0169232P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 PI Bienkowski MJ, Gurney M;
 XX
 DR WPI; 2001-444208/48.
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with amyloid
 PT precursor protein processing activity and alpha-secretase activity, for
 PT identifying modulators useful in treating Alzheimer's disease.
 XX
 PS Example 14; Page 155-156; 187pp; English.
 XX
 CC The patent discloses human aspartyl protease 1 (hu-Asp1) or modified Asp1
 CC proteins which lack transmembrane domain or amino terminal domain or
 CC cytoplasmic domain and retains alpha-secretase activity and amyloid
 CC protein precursor (APP) processing activity. The proteins of the
 CC invention are useful for assaying hu-Asp1 alpha-secretase activity, which
 CC in turn is useful for identifying modulators of hu-Asp1 alpha-secretase
 CC activity, where modulators that increase hu-Asp1 alpha-secretase activity
 CC are useful for treating Alzheimer's disease (AD) which causes progressive
 CC dementia with consequent formation of amyloid plaques, neurofibrillary
 CC tangles, gliosis and neuronal loss. Hu-Asp1 protease substrate is useful
 CC for assaying hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein
 CC with the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is human Asp 1 protein
 CC lacking a transmembrane (TM) domain and containing (His)6 tag. This
 CC sequence is generated from human Asp 1 protein by the deletion of its C-
 CC terminal TM domain and addition of hexa-histidine tag at its C-terminus
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 4; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.6e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60
 |
 Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60
 Qy 61 ALALEPALASPAGAAANFLAMVDNLQGD SGRGYYLEMLIGTPPQKLQILVD TGSSNFAVAG 120
 |
 Db 61 ALALEPALASPAGAAANFLAMVDNLQGD SGRGYYLEMLIGTPPQKLQILVD TGSSNFAVAG 120

Qy	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV	TIPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV	TIPKGFNTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA		240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA		240
Qy	241	GSQTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD	CREYNADKA	300
Db	241	GSQTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD	CREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFD	AVEAVARASLIPEFSDGFWTGSQ	LACWTNSETPWSYFPKISI 360
Db	301	IVDSGTTLLRLPQKVFD	AVEAVARASLIPEFSDGFWTGSQ	LACWTNSETPWSYFPKISI 360
Qy	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD		420
Db	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD		420
Qy	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG		480
Db	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG		480
Qy	481	AILLVLIVLLLLPFR	CQRRPRDPEVVNDESSLVRHRWK	518
Db	481	AILLVLIVLLLLPFR	CQRRPRDPEVVNDESSLVRHRWK	518

RESULT 10

AAE06858

ID AAE06858 standard; protein; 518 AA.

XX

AC AAE06858;

XX

DT 23-OCT-2001 (first entry)

XX

DE Human aspartyl protease 1 (Hu-Asp1) protein.

XX

KW Human; aspartyl protease 1; Asp 1; beta-amyloid precursor protein; APP;

KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;

KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;

KW neuroprotective; antisense therapy; gene therapy; chromosome 21.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .20
----	---------	--------

FT		/label= Signal_peptide
----	--	------------------------

FT	Protein	21. .518
----	---------	----------

FT		/note= "Mature human aspartyl protease 1 (Hu-Asp1)"
----	--	---

FT	Domain	469. .492
----	--------	-----------

FT		/label= Transmembrane_domain
----	--	------------------------------

XX

PN WO200150829-A2.

XX

PD 19-JUL-2001.

```

XX
PF 09-MAY-2001; 2001WO-IB000799.
XX
PR 09-MAY-2001; 2001WO-IB000799.
XX
PA (BIEN/) BIENKOWSKI M J.
PA (GURN/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX
PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
XX
DR WPI; 2001-483072/52.
DR N-PSDB; AAD13020.
XX
PT Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity.
XX
PS Example 2; Fig 1; 185pp; English.
XX
CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
CC precursor protein (APP) isoforms and their corresponding DNA molecules.
CC Human aspartyl proteases can act as beta-secretase proteases useful for
CC treating Alzheimer's disease. APP isoforms are useful for identifying
CC modulators of amyloid-beta peptide production, for use in designing
CC therapeutics for the treatment and prevention of Alzheimer's disease,
CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
CC and neuronal loss. APP isoforms are also used in methods for identifying
CC inhibitors and modulators of human Asp2 activity. The invention relates
CC to a method for identifying agents that modulate the activity of human
CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
CC as a means to screen in cellular assays for the inhibitors of beta- and
CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
CC polymerase chain reactions (PCR). The probes are useful for detecting Hu-
CC Asp nucleic acids in in vitro assays and in Northern and Southern blots.
CC The present sequence is human aspartyl protease 1 (Hu-Asp1). Hu-Asp 1
CC gene is localised on chromosome 21
XX
SQ Sequence 518 AA;

Query Match          100.0%;  Score 2687;  DB 4;  Length 518;
Best Local Similarity 100.0%;  Pred. No. 8.6e-231;
Matches 518;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60

Qy     61 ALALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ALALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy    121 TPHSYIDTYFDTERSSTYRSKGFVDTVKYTQGSWTGFGVGEDLVTIPKGFNTSFLVNIATI 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||

```

Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVITIPKGFNTSFLVNIATI 180
 Qy 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
 Qy 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLD CREYNADKA 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLD CREYNADKA 300
 Qy 301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
 Qy 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
 Qy 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
 Qy 481 AILLVLIVLLLLPFR CQRRPRDPEVVNDESSLVRHRWK 518
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 AILLVLIVLLLLPFR CQRRPRDPEVVNDESSLVRHRWK 518

RESULT 11

AAE02608

ID AAE02608 standard; protein; 518 AA.

XX

AC AAE02608;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human Aspartyl protease-1 (Asp-1) deltaTM (His)6 protein.

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;

KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Aspl;

KW beta-secretase; Asp-1 deltaTM (His)6 protein.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Gurney M, Bienkowski MJ;
 XX
 DR WPI; 2001-290516/30.
 XX
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease.
 XX
 PS Example 14; Page 183-184; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human Aspartyl protease-1
 CC (Asp-1) deltaTM (His)6 protein which is used for the expression of pre-
 CC pro-human-Aspartyl protease 1 (Asp1). This protein is obtained by
 CC replacing C-terminal transmembrane and cytoplasmic domains with a
 CC hexahistidine purification tag in the human Aspartyl protease 1
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 4; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.6e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPT	PGPGTPAERHADGL	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPT	PGPGTPAERHADGL	60
Qy	61	ALALEPALASPAGAAFLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAAFLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGF	DVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGF	DVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240	
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240	
Qy	241	GSGTNGGSLVLGGIEPSLYKGD	IWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Db	241	GSGTNGGSLVLGGIEPSLYKGD	IWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ	LACWTNSETPWSYFPKISI 360
Db	301	IVDSGTTLLRLPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ	LACWTNSETPWSYFPKISI 360
Qy	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420	
Db	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420	
Qy	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480	
Db	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480	

Qy 481 AILLVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518
 |||||
 Db 481 AILLVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518

RESULT 12

AAE02580

ID AAE02580 standard; protein; 518 AA.

XX

AC AAE02580;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human aspartyl protease 1 (Asp 1).

XX

KW Human; alpha-secretase; amyloid precursor protein; APP; therapy;

KW Alzheimer's disease; antialzheimer's; aspartyl protease 1; Asp 1;

KW beta-secretase; chromosome 21.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .20
----	---------	--------

FT		/label= Signal_peptide
----	--	------------------------

FT	Peptide	22. .62
----	---------	---------

FT		/label= Asp_1_prepropeptide
----	--	-----------------------------

FT	Peptide	23. .62
----	---------	---------

FT		/label= Asp_1_propeptide
----	--	--------------------------

FT	Protein	63. .518
----	---------	----------

FT		/label= Mature_human_Asp_1_protein
----	--	------------------------------------

FT		/note= "Specifically claimed"
----	--	-------------------------------

FT	Active-site	87. .89
----	-------------	---------

FT		/label= Active_site_1
----	--	-----------------------

FT	Active-site	110. .113
----	-------------	-----------

FT		/label= Active_site_2
----	--	-----------------------

FT	Active-site	303. .305
----	-------------	-----------

FT		/label= Active_site_3
----	--	-----------------------

FT	Domain	469. .492
----	--------	-----------

FT		/label= Transmembrane_domain
----	--	------------------------------

FT	Domain	493. .518
----	--------	-----------

FT		/label= Cytoplasmic_domain
----	--	----------------------------

FT	Region	497. .518
----	--------	-----------

FT		/note= "Peptide #1"
----	--	---------------------

XX

PN WO200123533-A2.

XX

PD 05-APR-2001.

XX

PF 22-SEP-2000; 2000WO-US026080.

XX

PR 23-SEP-1999; 99US-0155493P.

PR 23-SEP-1999; 99WO-US020881.

PR 13-OCT-1999; 99US-00416901.

PR 06-DEC-1999; 99US-0169232P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX
 PI Gurney M, Bienkowski MJ;
 XX
 DR WPI; 2001-290516/30.
 DR N-PSDB; AAD06738.
 XX
 PT Enzymes that cleave the alpha-secretase site of the amyloid precursor
 PT protein, useful for the treatment of Alzheimer's disease.
 XX
 PS Claim 29; Fig 1; 189pp; English.
 XX
 CC The present invention relates to enzymes for cleaving the alpha-
 CC secretase site of the amyloid precursor protein (APP) and methods of
 CC identifying those enzymes. The methods may be used to identify enzymes
 CC that may be used to cleave the alpha-secretase cleavage site of the APP
 CC protein. The enzymes may be used to treat or modulate the progress of
 CC Alzheimer's disease. The present sequence is human aspartyl protease 1
 CC (Asp 1). Asp 1 has alpha-secretase protease and beta-secretase protease
 CC activities. Asp 1 gene is located on chromosome 21
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 4; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.6e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPT	PGPGTPAERHADGL	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPT	PGPGTPAERHADGL	60
Qy	61	ALALEPALASPAGAAFLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAAFLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGF	DVTVKYTQGSWTGFVGEDLV	180
Db	121	TPHSYIDTYFDTERSSTYRSKGF	DVTVKYTQGSWTGFVGEDLV	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFD	SLVTQANIPNVFSMQMCGAGLPVA	240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFD	SLVTQANIPNVFSMQMCGAGLPVA	240
Qy	241	GSGTNGGSLVLGGIEPSLYKGD	IWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Db	241	GSGTNGGSLVLGGIEPSLYKGD	IWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ	360
Db	301	IVDSGTTLLRLPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ	360
Qy	361	YLRDENSSRSFRITILPQLYIQ	PMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Db	361	YLRDENSSRSFRITILPQLYIQ	PMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Qy	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTED	VASNCVPAQSLSEPILWIVSYALMSVCG	480
Db	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTED	VASNCVPAQSLSEPILWIVSYALMSVCG	480

QY 481 AILLVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518
 |||||
 Db 481 AILLVLIVLLLLPFCQRRPRDPEVVNDESSLVRHRWK 518

RESULT 13

AAU29059

ID AAU29059 standard; protein; 518 AA.

XX

AC AAU29059;

XX

DT 18-DEC-2001 (first entry)

XX

DE Human PRO polypeptide sequence #36.

XX

KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200168848-A2.

XX

PD 20-SEP-2001.

XX

PF 28-FEB-2001; 2001WO-US006520.

XX

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.

PR 06-MAR-2000; 2000US-0186968P.

PR 14-MAR-2000; 2000US-0189320P.

PR 14-MAR-2000; 2000US-0189328P.

PR 15-MAR-2000; 2000WO-US006884.

PR 21-MAR-2000; 2000US-0190828P.

PR 21-MAR-2000; 2000US-0191007P.

PR 21-MAR-2000; 2000US-0191048P.

PR 21-MAR-2000; 2000US-0191314P.

PR 28-MAR-2000; 2000US-0192655P.

PR 29-MAR-2000; 2000US-0193032P.

PR 29-MAR-2000; 2000US-0193053P.

PR 30-MAR-2000; 2000WO-US008439.

PR 04-APR-2000; 2000US-0194449P.

PR 04-APR-2000; 2000US-0194647P.

PR 11-APR-2000; 2000US-0195975P.

PR 11-APR-2000; 2000US-0196000P.

PR 11-APR-2000; 2000US-0196187P.

PR 11-APR-2000; 2000US-0196690P.

PR 11-APR-2000; 2000US-0196820P.

PR 18-APR-2000; 2000US-0198121P.

PR 18-APR-2000; 2000US-0198585P.

PR 25-APR-2000; 2000US-0199397P.

PR 25-APR-2000; 2000US-0199550P.

PR 25-APR-2000; 2000US-0199654P.

PR 03-MAY-2000; 2000US-0201516P.

Qy	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGNTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFD SLVTQANIPNVFSMQMCGAGLPVA	240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFD SLVTQANIPNVFSMQMCGAGLPVA	240
Qy	241	GS GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Db	241	GS GTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFD AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLLRLPQKVFD AVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI	360
Qy	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Db	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Qy	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCG	480
Db	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCG	480
Qy	481	AILLV LIVLLLLPFCRRPRDPEVVNDESSLVRHRWK	518
Db	481	AILLV LIVLLLLPFCRRPRDPEVVNDESSLVRHRWK	518

RESULT 14

AAU06602

ID AAU06602 standard; protein; 518 AA.

XX

AC AAU06602;

XX

DT 24-OCT-2001 (first entry)

XX

DE Human Aspartyl protease 1 (Asp1).

XX

KW Human; Aspartyl protease; Asp1; Asp2; beta-secretase; nootropic;
 KW neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
 KW amyloid-beta; Abeta.

XX

OS Homo sapiens.

XX

PN WO200149098-A2.

XX

PD 12-JUL-2001.

XX

PF 09-MAY-2001; 2001WO-IB000798.

XX

PR 09-MAY-2001; 2001WO-IB000798.

XX

PA (BIEN/) BIENKOWSKI M J.

PA (GURN/) GURNEY M E.

PA (HEIN/) HEINRIKSON R L.

PA (PARO/) PARODI L A.

PA (YANR/) YAN R.
 XX
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX
 DR WPI; 2001-502549/55.
 DR N-PSDB; AAS11516.
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity.
 XX
 PS Example 2; Fig 1; 185pp; English.
 XX
 CC The invention relates to a purified polypeptide comprising a fragment of
 CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
 CC transmembrane domain and the Asp2 protein, and where the polypeptide and
 CC the fragment retain the beta-secretase activity of the mammalian Asp2
 CC protein. The invention also details polynucleotides for the Asp proteins
 CC and vectors expressing them, and a polypeptide (isoform of amyloid
 CC protein precursor (APP)) comprising the amino acid sequence of an APP or
 CC its fragment containing an APP cleavage site recognizable by a mammalian
 CC beta-secretase, and further comprising two lysine residues at the
 CC carboxyl terminus of the amino acid sequence of the mammalian APP or APP
 CC fragment. Also included in the invention are methods of identifying
 CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
 CC useful for treating Alzheimer's disease. APP is useful in methods for
 CC identifying inhibitors or modulators of human Asp2 activity and amyloid-
 CC beta (Abeta) peptide production. APP is also useful in designing
 CC therapeutics for the treatment or prevention of Alzheimer's disease. APP
 CC comprising the APP-Sw-beta-secretase peptide sequence (NLDA), which is
 CC associated with increased levels of Abeta processing is useful in assays
 CC relating the Alzheimer's research. The expression vector is useful for
 CC recombinantly expressing APP. Nucleic acids that hybridise to Asp
 CC oligonucleotides are useful as probes or primers. The probes are useful
 CC for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and
 CC Southern blots. The present sequence is human Asp1
 XX
 SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 4; Length 518;
 Best Local Similarity 100.0%; Pred. No. 8.6e-231;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTTPGPGTPAERHADGL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTTPGPGTPAERHADGL 60

 Qy 61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

 Qy 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATI 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATI 180

 Qy 181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

```

      |||
Db      181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVA 240
Qy      241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300
      |||
Db      241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300
Qy      301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
      |||
Db      301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
Qy      361 YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
      |||
Db      361 YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
Qy      421 RAQKRVGFASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCG 480
      |||
Db      421 RAQKRVGFASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCG 480
Qy      481 AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK 518
      |||
Db      481 AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK 518

```

RESULT 15

ABB06531

ID ABB06531 standard; protein; 518 AA.

XX

AC ABB06531;

XX

DT 31-MAY-2002 (first entry)

XX

DE Human aspartyl protease 1 protein SEQ ID NO:125.

XX

KW Beta-secretase; enzyme; cleavage site; amyloid protein precursor; APP;
 KW aspartyl protease; neuroprotective; nootropic; beta-secretase inhibitor;
 KW Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200206306-A2.

XX

PD 24-JAN-2002.

XX

PF 19-JUL-2001; 2001WO-US023035.

XX

PR 19-JUL-2000; 2000US-0219795P.

PR 12-MAR-2001; 2001US-0275251P.

XX

PA (PHAA) PHARMACIA & UPJOHN CO.

XX

PI Yan R, Tomasselli AG, Gurney ME, Emmons TL, Bienkowski MJ;
 PI Heinrikson RL;

XX

DR WPI; 2002-216995/27.

XX

PT Novel substrates for human aspartyl protease useful for identifying

PT modulators of beta secretase activity of aspartyl protease for treating
PT Alzheimer's disease.

XX

PS Disclosure; Page 161-162; 188pp; English.

XX

CC The present invention describes an isolated peptide (I) comprising a
CC sequence of at least four amino acids, where the peptide is a substrate
CC for conducting aspartyl protease assays. (I) has neuroprotective and
CC nootropic activities, and can be used as an inhibitor of beta-secretase
CC activity. A beta-secretase modulator from the present invention can be
CC used for inhibiting beta-secretase activity in vivo, and in the
CC manufacture of a medicament for the treatment of Alzheimer's disease.
CC Pharmaceutical compositions from the present invention can be used for
CC treating a disease or condition characterised by an abnormal beta-
CC secretase activity. (I) is useful for identifying agents that modulate
CC the activity of human Asp2 aspartyl protease (Hu-Asp2). (I) is useful as
CC a core structure to construct derivatives. ABL49914 to ABL49925 and
CC ABB06409 to ABB06593 represent sequences used in the exemplification of
CC the present invention

XX

SQ Sequence 518 AA;

Query Match 100.0%; Score 2687; DB 5; Length 518;
Best Local Similarity 100.0%; Pred. No. 8.6e-231;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTTPGPGTPAERHADGL 60
|
Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTTPGPGTPAERHADGL 60

Qy 61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
|
Db 61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
|
Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180

Qy 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
|
Db 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
|
Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300

Qy 301 IVDSGTTLRLRPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
|
Db 301 IVDSGTTLRLRPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360

Qy 361 YLRDENSSRSFRITILPQLYIQPMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
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Db 361 YLRDENSSRSFRITILPQLYIQPMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy 421 RAQKRVGFAASPCAIEIAGAASVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
|
Db 421 RAQKRVGFAASPCAIEIAGAASVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

Qy 481 AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK 518
 |||||
Db 481 AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK 518

Search completed: February 28, 2004, 09:09:16
Job time : 64.4242 secs

OM protein - protein search, using sw model

Run on: February 28, 2004, 09:08:05 ; Search time 18.5 Seconds
(without alignments)
1445.527 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALARALLPLLAQWLLRA.....RPRDPEVVNDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
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1	2687	100.0	518	3	US-08-999-723-2	Sequence 2, Appli	
2	2687	100.0	518	3	US-09-434-427-2	Sequence 2, Appli	
3	2687	100.0	518	4	US-09-548-372D-2	Sequence 2, Appli	
4	2687	100.0	518	4	US-09-548-367D-2	Sequence 2, Appli	
5	2687	100.0	518	4	US-09-551-853D-2	Sequence 2, Appli	
6	2687	100.0	518	4	US-09-215-450-19	Sequence 19, Appl	
7	2395	89.1	514	3	US-09-717-432-2	Sequence 2, Appli	
8	2395	89.1	514	4	US-09-912-484-2	Sequence 2, Appli	
9	1186.5	44.2	501	4	US-09-713-158-2	Sequence 2, Appli	
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12	1185	44.1	501	4	US-09-551-853D-8	Sequence 8, Appli
13	1184.5	44.1	501	4	US-09-724-566A-65	Sequence 65, Appl
14	1178.5	43.9	501	4	US-09-548-372D-4	Sequence 4, Appli
15	1178.5	43.9	501	4	US-09-548-367D-4	Sequence 4, Appli
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17	1178.5	43.9	501	4	US-09-724-566A-2	Sequence 2, Appli
18	1175	43.7	488	4	US-09-604-608-2	Sequence 2, Appli
19	1175	43.7	503	4	US-09-604-608-3	Sequence 3, Appli
20	1172.5	43.6	501	4	US-09-009-191-2	Sequence 2, Appli
21	1171.5	43.6	456	4	US-09-724-566A-43	Sequence 43, Appl
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34	1132	42.1	431	4	US-09-724-566A-74	Sequence 74, Appl
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37	1127	41.9	433	4	US-09-548-367D-26	Sequence 26, Appl
38	1127	41.9	433	4	US-09-551-853D-26	Sequence 26, Appl
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41	1127	41.9	446	4	US-09-551-853D-22	Sequence 22, Appl
42	1127	41.9	459	4	US-09-548-372D-24	Sequence 24, Appl
43	1127	41.9	459	4	US-09-548-367D-24	Sequence 24, Appl
44	1127	41.9	459	4	US-09-551-853D-24	Sequence 24, Appl
45	1124	41.8	420	4	US-09-724-566A-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
 US-08-999-723-2
 ; Sequence 2, Application US/08999723A
 ; Patent No. 6025180
 ; GENERAL INFORMATION:
 ; APPLICANT: Powell, David J.
 ; APPLICANT: Southan, Christopher
 ; APPLICANT: Chapman, Conrad G.
 ; APPLICANT: Evans, Joanne R.
 ; TITLE OF INVENTION: ASPl
 ; FILE REFERENCE: GH70262
 ; CURRENT APPLICATION NUMBER: US/08/999,723A
 ; CURRENT FILING DATE: 1997-10-06
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 518
 ; TYPE: PRT

; ORGANISM: Homo sapiens
US-08-999-723-2

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Query Match          100.0%; Score 2687; DB 3; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.2e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60

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Db      241 GSGTNGGSLVLGGIEPSLYKGD IWTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300

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Db      301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360

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RESULT 2
US-09-434-427-2
; Sequence 2, Application US/09434427
; Patent No. 6162630
; GENERAL INFORMATION:
; APPLICANT: POWELL, DAVID J.
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: CHAPMAN, CONRAD G.
; APPLICANT: EVANS, JOANNE R.
; TITLE OF INVENTION: ASP1
; FILE REFERENCE: GH-70262-D1
; CURRENT APPLICATION NUMBER: US/09/434,427
; CURRENT FILING DATE: 1999-11-04

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; EARLIER APPLICATION NUMBER: US 08/999,723
; EARLIER FILING DATE: 1997-10-06
; EARLIER APPLICATION NUMBER: UK 9626022.9
; EARLIER FILING DATE: 1996-12-14
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-434-427-2

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Query Match          100.0%; Score 2687; DB 3; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.2e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTTPGPGTPAERHADGL 60

Qy     61 ALALEPALASPAGAAFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
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Db     61 ALALEPALASPAGAAFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

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Db    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180

Qy    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLD CREYNADKA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLD CREYNADKA 300

Qy    301 IVDSGTLLRLRPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
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Qy    361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
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Db    361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy    421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
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Db    421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

Qy    481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
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Db    481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518

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RESULT 3
US-09-548-372D-2
; Sequence 2, Application US/09548372D
; Patent No. 6420534

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; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280I
; CURRENT APPLICATION NUMBER: US/09/548,372D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-372D-2

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Query Match          100.0%; Score 2687; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.2e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGBTAPERHADGL 60

Qy     61 ALALEPALASPAGAAFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
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Qy    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATI 180
|
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Qy    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
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Db    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300
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Qy    301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
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Db    301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360

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Db    361 YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy    421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

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Db          421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
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RESULT 4

US-09-548-367D-2

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; Sequence 2, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-367D-2

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Query Match          100.0%; Score 2687; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.2e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPPTAERHADGL 60
Qy          61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Db          61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Qy          121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
Db          121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
Qy          181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
Db          181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
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RESULT 5

US-09-551-853D-2

; Sequence 2, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 518

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-551-853D-2

Query Match 100.0%; Score 2687; DB 4; Length 518;

Best Local Similarity 100.0%; Pred. No. 2.2e-243;

Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 ALALEPALASPAGAAANFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
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Db      121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATI 180
Qy      181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
Db      181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
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Qy      361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTN ALVIGATVMEGFYVIFD 420
Db      361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTN ALVIGATVMEGFYVIFD 420
Qy      421 RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSL SEPILWIVSYALMSVCG 480
Db      421 RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSL SEPILWIVSYALMSVCG 480
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Db      481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518

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RESULT 6

US-09-215-450-19

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; Sequence 19, Application US/09215450
; Patent No. 6635748
; GENERAL INFORMATION:
; APPLICANT: Giese, Klaus
; APPLICANT: Xin, Hong
; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES
; FILE REFERENCE: 1451.100 / 210030.447
; CURRENT APPLICATION NUMBER: US/09/215,450
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 518
; TYPE: PRT
; ORGANISM: human

```

US-09-215-450-19

```

Query Match          100.0%; Score 2687; DB 4; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.2e-243;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||

```


Query Match 89.1%; Score 2395; DB 3; Length 514;
 Best Local Similarity 88.6%; Pred. No. 5.6e-216;
 Matches 459; Conservative 20; Mismatches 35; Indels 4; Gaps 1;

```

Qy      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPGPGTPAERHADGL 60
      |||| |||| :|||| | | |||||:| || | : || ||| ||||
Db      1 MGALLRALLLVLAQWLLSAVPALAPAPFTLPLQVAGATNHRASAVPGLGTPELPRADGL 60

Qy     61 ALALEPALASPAGAAFLAMVDNLQDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
      ||||| |: |||||:|||||:|||||:|||||:|||||
Db     61 ALALEPVRAT----ANFLAMVDNLQDGRGYYLEMLIGTPPQKVQILVDTGSSNFAVAG 116

Qy    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATI 180
      |||||:| ||| |||||:|||||:|||||:|||||:|||||
Db    117 APHSYIDTYFDSESSSTYHSKGFDTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATI 176

Qy    181 FESENFPLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFSMQMCGAGLPVA 240
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    177 FESENFPLPGIKWNGILGLAYAAALAKPSSSLETFFDLSLVAQAKIPDIFSMQMCAGLPVA 236

Qy    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLD CREYNADKA 300
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    237 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLD CREYNADKA 296

Qy    301 IVDSGTLLRLRPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    297 IVDSGTLLRLRPQKVFD AVEAVARTSLIPEFSDGFWTGAQLACWTNSETPWAYFPKISI 356

Qy    361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
      |||||:|||||:|||||:|||||:|||||:|||||:|||||
Db    357 YLRDENASRSFRITILPQLYIQPMMGAGFNYECYRFGISSSTNALVIGATVMEGFYVIFD 416

Qy    421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
      |||:|||| | ||| | |||||:|||||:|||||:|||||
Db    417 RAQRRVGFAVSPCAIEGTTVSEISGPFSTEDIASNCVPAQALNEPILWIVSYALMSVCG 476

Qy    481 AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK 518
      |||||:|||| |: |||||:|||||
Db    477 AILLVLIVLLLLPLHCRHAPRDPEVVNDESSLVRHRWK 514

```

RESULT 8

US-09-912-484-2

; Sequence 2, Application US/09912484

; Patent No. 6358725

; GENERAL INFORMATION:

; APPLICANT: Christie, Gary

; APPLICANT: Li, Xiaotong

; APPLICANT: Powell, David J.

; APPLICANT: Zhu, Yuan

; TITLE OF INVENTION: Mouse Aspartic Secretase-1 (mASP1)

; FILE REFERENCE: GP-70663-D1

; CURRENT APPLICATION NUMBER: US/09/912,484

; CURRENT FILING DATE: 2001-07-25

; PRIOR APPLICATION NUMBER: 60/166,974

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: 09/717,432
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 514
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-912-484-2

Query Match 89.1%; Score 2395; DB 4; Length 514;
Best Local Similarity 88.6%; Pred. No. 5.6e-216;
Matches 459; Conservative 20; Mismatches 35; Indels 4; Gaps 1;

```
Qy      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTTPGPGTPAERHADGL 60
      ||||| ||||| : ||||| | | ||||| ||||| : || ||| |||||
Db      1 MGALLRALLLLVLAQWLLSAVPALAPAPFTLPLQVAGATNHRASAVPGLGTPELPRADGL 60

Qy     61 ALALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
      ||||| | : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 ALALEPV RAT-----ANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKVQILVDTGSSNFAVAG 116

Qy    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATI 180
      ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    117 APHSYIDTYFDSESSSTYHSGFDTVKYTQGSWTGFVGEDLV TIPKGFNSSFLVNIATI 176

Qy    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    177 FESENFFLPGIKWNGILGLAYAAALAKPSSSLETFFDSLVAQAKIPDIFSMQMCGAGLPVA 236

Qy    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    237 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 296

Qy    301 IVDSGTTLRLRPQKVFD AVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKISI 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    297 IVDSGTTLRLRPQKVFD AVEAVARTSLIPEFSDGFWTGAQLACWTNSETPWAYFPKISI 356

Qy    361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    357 YLRDENASRSFRITILPQLYIQPMMGAGFNYECYRFGISSSTNALVIGATVMEGFYVIFD 416

Qy    421 RAQKRVGFAASPCAIEIAGA AVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
      ||| : ||||| ||||| | ||||| ||||| : ||||| : ||||| ||||| |||||
Db    417 RAQRRVGFAVSPCAIEIGTTVSEISGPFSTEDIASNCVPAQALNEPILWIVSYALMSVCG 476

Qy    481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
      ||||| : ||||| | : ||||| ||||| ||||| ||||| ||||| |||||
Db    477 AILLVLIVLLLLPLHCRHAPRDPEVVNDESSLVRHRWK 514
```

RESULT 9
US-09-713-158-2
; Sequence 2, Application US/09713158
; Patent No. 6361975
; GENERAL INFORMATION:
; APPLICANT: ZHU, YUAN

```
; APPLICANT: LI, XIAOTONG
; APPLICANT: POWELL, DAVID J.
; APPLICANT: CHRISTIE, GARY
; TITLE OF INVENTION: MOUSE ASPARTIC SECRETASE-2 (MASP-2)
; FILE REFERENCE: GP-70660
; CURRENT APPLICATION NUMBER: US/09/713,158
; CURRENT FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 60/165,800
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 501
; TYPE: PRT
; ORGANISM: MUS MUSCULUS
US-09-713-158-2
```

```
Query Match          44.2%; Score 1186.5; DB 4; Length 501;
Best Local Similarity 46.0%; Pred. No. 1.4e-102;
Matches 238; Conservative 83; Mismatches 167; Indels 29; Gaps 8;
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```
Qy      7 ALLLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTGPGPCTPAERHADGLA 61
      | ||| | |:      : || | ||| | | | | | | :
Db      2 AQALPWLLLWV---GSGMLPAQGTHLGIRLPLRSGLA-----GPPLGLRLPRETDEES-- 51

Qy     62 LALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGT 121
      |      :|: |||||:| ||:||||:| |:||| | |||||
Db     52 -----EPPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFAVGAA 104

Qy    122 PHSYIDTYFDTERSSTYRSKGFVDTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIF 181
      || :: | : : |||| | | |||| | | :| |||:| | | : ||| |
Db    105 PHPFLHRYYQRQLSSTYRDLRKGVPYVPYQGWEGELGTDIVSIPHGPNTVVRANIAAIT 164

Qy    182 ESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDLSLVTQANIPNVFMSQMCGAGLPV-- 239
      ||: ||: | | ||||| ||:| ||| ||||| | :|||:| |:| ||| |:
Db    165 ESKDFFINGSNWEGILGLAYAEIARPDSSLEPFDFSLVKQTHIPNIFSLQLCGAGFPLNQ 224

Qy    240 -AGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNAD 298
      : |||:::| | | ||| | :|||: | |||: | :|:| | | :|:| | |
Db    225 TEALASVGGSMTIIGGDHSLYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYD 284

Qy    299 KAIVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKI 358
      |:| ||||| ||||:| |:| :| ||| | || | | |||: | | |
Db    285 KSIIVDSGTTNLRPLPKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVI 344

Qy    359 SIYLRDENSSRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYV 417
      |:| | | ::| ||||| | |:| : | :|:| | | : | :|:| | | |
Db    345 SLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYV 404

Qy    418 IFDRAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMS 477
      :|||:| |:| | | : : ||| | |: | | | :| : :
Db    405 VFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTDAMEDCGYNIPQTDDESTLMTIAYVMAA 464

Qy    478 VCGAILLVLLIVLLLLPFRQCR--RPRDPEVVNDESSL 512
      :| |: : : |: : || | | : : :| | |
Db    465 IC-ALFMLPLCLMVCQWRCLRCLRHQHDDFADDISLL 500
```

RESULT 10
 US-09-548-372D-8
 ; Sequence 8, Application US/09548372D
 ; Patent No. 6420534
 ; GENERAL INFORMATION:
 ; APPLICANT: GURNEY ET AL.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 29915/6280I
 ; CURRENT APPLICATION NUMBER: US/09/548,372D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-548-372D-8

Query Match 44.1%; Score 1185; DB 4; Length 501;
 Best Local Similarity 46.0%; Pred. No. 1.9e-102;
 Matches 237; Conservative 83; Mismatches 169; Indels 26; Gaps 7;

Qy	9	LLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTPGPGTPAERHADGLALA	63
		: : :	
Db	1	MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLA-----GPPLGLRLPRETDEES----	51
Qy	64	LEPALASPAGAAANFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPH	123
		: : : : : :	
Db	52	-----EPPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAAPH	106
Qy	124	SYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFES	183
		: : : : :	
Db	107	PFLHRYYQRLSSSTYRDLRKGVYPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITES	166
Qy	184	ENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV---A	240
		: : : : : : :	
Db	167	DKFFINGSNWEGLGLAYAEIARPDSDLPPFFDSLQTHIPNIFSLQLCGAGFPLNQTE	226
Qy	241	SGGTNGGSLVLGGIEPSLYKGDWYTPIKEEYQIEILKLEIGGQSLNLDREYNADKA	300
		: : : : : : : : : :	
Db	227	ALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDKS	286
Qy	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
		: : :	
Db	287	IVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISL	346

Qy 361 YLRDENSSRSFRITILPQLYIQPMAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIF 419
 || | ::||| ||| |::| : :||:| :| | :| | :||| ||:|
 Db 347 YLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVF 406
 Qy 420 DRAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVC 479
 |||:|:| | | : : || | | : | | :| : :|
 Db 407 DRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAAIC 466
 Qy 480 GAILLVLLVLLLLPFRQR--RPRDPEVVNDESSL 512
 |: :: : |:: :|| | | : : :| | |
 Db 467 -ALFMLPLCLMVCQWRCRLRCLRHQHDDFADDISLL 500

RESULT 11

US-09-548-367D-8

; Sequence 8, Application US/09548367D
 ; Patent No. 6440698
 ; GENERAL INFORMATION:
 ; APPLICANT: GURNEY ET AL.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 29915/6280H
 ; CURRENT APPLICATION NUMBER: US/09/548,367D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-548-367D-8

Query Match 44.1%; Score 1185; DB 4; Length 501;
 Best Local Similarity 46.0%; Pred. No. 1.9e-102;
 Matches 237; Conservative 83; Mismatches 169; Indels 26; Gaps 7;

Qy 9 LLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTGPPTPAERHADGLALA 63
 : | | | : || | | | | | | :
 Db 1 MAPALHWLLWVGSGMLPAQGTHLGIRLPLRSGLA-----GPPLGLRLPRETDEES---- 51
 Qy 64 LEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPH 123
 | :|: ||||:| ||:|:| | :|:| | | | | | | | |
 Db 52 -----EPPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPPTLNILVDTGSSNFAVGAAPH 106
 Qy 124 SYIDTYFDTERSSTYRSKGFVDVTVKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATIFES 183
 :: | : |||| | | |||| | | : |||| | | : |||| | |
 Db 107 PFLHRYYQRQLSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITES 166

Qy 184 ENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV---A 240
 : ||: | | ||||| :|:| ||| ||||| | :||:|:|:| ||: |:
 Db 167 DKFFINGSNWEGILGLAYAEIARPPDSLEPFDSLQTHIPNIFSLQLCGAGFPLNQTE 226

Qy 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDREYNADKA 300
 : ||:|:|:|:| ||| | :|||:| |||:| :|:| || | :||:| ||: |:
 Db 227 ALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDKS 286

Qy 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
 ||||| ||||:|:| | :|:| || | ||| | ||| | ||: | ||: |:
 Db 287 IVDSGTTNLRPLPKVFEEAAVKSIAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISL 346

Qy 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIF 419
 || | :|:| ||||| | :|:| : :|:| :| | : | :| :|||:| |:
 Db 347 YLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVF 406

Qy 420 DRAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVC 479
 ||:|:|:| | | : : ||| | | : | | :| : :| |:
 Db 407 DRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAAIC 466

Qy 480 GAILLVLIVLLLLPFRQCR--RPRDPEVVNDESSL 512
 | : : : | : : | | | : : : | | |
 Db 467 -ALFMLPLCLMVCQWRCLRLRHQHDDFADDISL 500

RESULT 12

US-09-551-853D-8

; Sequence 8, Application US/09551853D

; Patent No. 6500667

; GENERAL INFORMATION:

; APPLICANT: GURNEY ET AL.

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 29915/6280L

; CURRENT APPLICATION NUMBER: US/09/551,853D

; CURRENT FILING DATE: 2000-04-18

; PRIOR APPLICATION NUMBER: US 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: US 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 501

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-551-853D-8

Query Match 44.1%; Score 1185; DB 4; Length 501;

Best Local Similarity 46.0%; Pred. No. 1.9e-102;

Matches 237; Conservative 83; Mismatches 169; Indels 26; Gaps 7;


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; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-724-566A-65
```

```
Query Match          44.1%; Score 1184.5; DB 4; Length 501;
Best Local Similarity 45.9%; Pred. No. 2.1e-102;
Matches 237; Conservative 84; Mismatches 170; Indels 25; Gaps 7;
```

```
Qy      9 LLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTPGPGTPAERHADGLALA 63
      : | |  ||      : | |  |  |||  |  |  |  |  |  :
Db      1 MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLA-----GPPLGLRLPRETDEES---- 51

Qy     64 LEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPH 123
      |      :|: |||||:| ||:||||:| |:||| | ||||| ||
Db     52 -----EPPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAAPH 106

Qy    124 SYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFES 183
      :: | :  : ||||  | | |||  | | :| |||:| | | :  || | ||
Db    107 PFLHRYYQRLSSTYRDLRGKVYVPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITES 166

Qy    184 ENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFMSMQMCGAGLPV---A 240
      : ||: |  | ||||| ||:| | | ||||| | :|||:| |:| ||| | :
Db    167 DKFFINGSNWEGLGLAYAEIARPDSDLPPFDLSLVKQTHIPNIFSLQLCGAGFPLNQTE 226

Qy    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWWYQIEILKLEIGGQSLNLDREYNADKA 300
      : |||:::| | : || | : ||||: ||||: |::| | | : ||: || | :
Db    227 ALASVGGSMTIIGDHSLYTGSWYTPIRREWYEVIVRVEINGQDLKMDCKEYNYDKS 286

Qy    301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
      ||||| ||||:| |:| |:: | | : | ||| | || | | |||: || ||:
Db    287 IVDSGTTNLRPLPKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISL 346

Qy    361 YLRDENSSRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIF 419
      || | :::||| |||| |::| : : ||: | : | : | : || : |||||:|
Db    347 YLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVF 406

Qy    420 DRAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVC 479
      |||:| |:| | | : : || | | : | | | : | : | : | : |
Db    407 DRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAAIC 466

Qy    480 GAILLVLIIVLLLPPFRCQRRPR-DPEVVNDESSLVR 514
      | : : : | : : : || | | : | : | : | :
Db    467 -ALFMLPLCLMVCQWRCLRLRHQHDDFGDDISLLK 501
```


US-09-548-372D-4
 ; Sequence 4, Application US/09548372D
 ; Patent No. 6420534
 ; GENERAL INFORMATION:
 ; APPLICANT: GURNEY ET AL.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 29915/6280I
 ; CURRENT APPLICATION NUMBER: US/09/548,372D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-548-372D-4

Query Match 43.9%; Score 1178.5; DB 4; Length 501;
 Best Local Similarity 46.2%; Pred. No. 7.8e-102;
 Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;

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US-09-548-367D-4

; Sequence 4, Application US/09548367D
 ; Patent No. 6440698
 ; GENERAL INFORMATION:
 ; APPLICANT: GURNEY ET AL.
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
 AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: 29915/6280H
 ; CURRENT APPLICATION NUMBER: US/09/548,367D
 ; CURRENT FILING DATE: 2000-04-12
 ; PRIOR APPLICATION NUMBER: US 60/155,493
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 09/404,133
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: PCT/US99/20881
 ; PRIOR FILING DATE: 1999-09-23
 ; PRIOR APPLICATION NUMBER: US 60/101,594
 ; PRIOR FILING DATE: 1998-09-24
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 501
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-548-367D-4

Query Match 43.9%; Score 1178.5; DB 4; Length 501;
 Best Local Similarity 46.2%; Pred. No. 7.8e-102;
 Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;

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 Job time : 19.5 secs

OM protein - protein search, using sw model

Run on: February 28, 2004, 09:11:20 ; Search time 33.6364 Seconds
(without alignments)
3251.760 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
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Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

8

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No.	Score	Match	Length	DB	ID		Description

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2	2687	100.0	518	9	US-09-795-847-2	Sequence 2, Appli
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4	2687	100.0	518	9	US-09-794-748-2	Sequence 2, Appli
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6	2687	100.0	518	9	US-09-215-450-19	Sequence 19, Appl
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8	2687	100.0	518	9	US-09-978-295A-196	Sequence 196, App
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ALIGNMENTS

RESULT 1
 US-09-794-927-2
 ; Sequence 2, Application US/09794927
 ; Patent No. US20010016324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gurney, Mark E.

```

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927-2

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Query Match          100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.8e-240;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-795-847-2

; Sequence 2, Application US/09795847

; Patent No. US20010018208A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
 AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280DE

; CURRENT APPLICATION NUMBER: US/09/795,847

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594

; PRIOR FILING DATE: 1998-09-24

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 518

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-795-847-2

Query Match 100.0%; Score 2687; DB 9; Length 518;

Best Local Similarity 100.0%; Pred. No. 2.8e-240;

Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 2, Application US/09794743

; Patent No. US20010021391A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND

; TITLE OF INVENTION: USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280BC

; CURRENT APPLICATION NUMBER: US/09/794,743

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 09/416,901

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; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-743-2

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.8e-240;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
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Db    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180

Qy    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDCREYNADKA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDCREYNADKA 300

Qy    301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360

Qy    361 YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy    421 RAQKRVGFAASPCAIEIAGAASEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 RAQKRVGFAASPCAIEIAGAASEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

Qy    481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
        ||||||||||||||||||||||||||||||||||||
Db    481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
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RESULT 4
US-09-794-748-2
; Sequence 2, Application US/09794748
; Patent No. US20020037315A1
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.

```

; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Riqiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR,
AND
; TITLE OF INVENTION: USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 28341/6280JL
; CURRENT APPLICATION NUMBER: US/09/794,748
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-748-2

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Query Match          100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.8e-240;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPATPAERHADGL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPATPAERHADGL 60

Qy     61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVITPKGFNTSFLVNIATI 180

Qy    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300

Qy    301 IVDSGTTLRLRPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 IVDSGTTLRLRPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360

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Db          61 ALALEPALASPAGAAFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
Qy          121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATI 180
            |||
Db          121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIATI 180
Qy          181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
            |||
Db          181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
Qy          241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300
            |||
Db          241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300
Qy          301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
            |||
Db          301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
Qy          361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
            |||
Db          361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
Qy          421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCG 480
            |||
Db          421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCG 480
Qy          481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
            |||
Db          481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518

```

RESULT 6

US-09-215-450-19

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; Sequence 19, Application US/09215450
; Patent No. US20020068278A1
; GENERAL INFORMATION:
; APPLICANT: Giese, Klaus
; APPLICANT: Xin, Hong
; TITLE OF INVENTION: METASTATIC BREAST AND COLON CANCER REGULATED GENES
; FILE REFERENCE: 1451.100 / 210030.447
; CURRENT APPLICATION NUMBER: US/09/215,450
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 518
; TYPE: PRT
; ORGANISM: human
US-09-215-450-19

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Query Match          100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.8e-240;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60
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Db          1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60

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Qy 61 ALALEPALASPAGAAFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ALALEPALASPAGAAFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGNTSFLVNIATI 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGNTSFLVNIATI 180

Qy 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300

Qy 301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360

Qy 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy 421 RAQKRVGFAASPCAIEIAGA AVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCG 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 RAQKRVGFAASPCAIEIAGA AVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCG 480

Qy 481 AILLVLIVLLLLPFR CQRRPRDPEVND ESSLVRHRWK 518
 ||||||||||||||||||||||||||||||||||||||||
 Db 481 AILLVLIVLLLLPFR CQRRPRDPEVND ESSLVRHRWK 518

RESULT 7

US-09-681-442-2

; Sequence 2, Application US/09681442

; Patent No. US20020081634A1

; GENERAL INFORMATION:

; APPLICANT: Gurney, Mark E.

; APPLICANT: Bienkowski, Michael J.

; APPLICANT: Heinrikson, Robert L.

; APPLICANT: Parodi, Luis A.

; APPLICANT: Yan, Riqiang

; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES

; TITLE OF INVENTION: THEREFOR

; FILE REFERENCE: 28341/6280FG

; CURRENT APPLICATION NUMBER: US/09/681,442

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 09/416,901

; PRIOR FILING DATE: 1999-10-13

; PRIOR APPLICATION NUMBER: 60/155,493

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: 09/404,133

; PRIOR FILING DATE: 1999-09-23

; PRIOR APPLICATION NUMBER: PCT/US99/20881

; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-681-442-2

Query Match 100.0%; Score 2687; DB 9; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.8e-240;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPT	PGPGT	PAERHADGL	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPT	PGPGT	PAERHADGL	60
Qy	61	ALALEPALASPAGAAFLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120	
Db	61	ALALEPALASPAGAAFLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120	
Qy	121	TPHSYIDTYFDTERSSTYRSKGF	DVTVKYTQGSWTG	FGVGEDLV	TIPKGFNTSFLVNIATI 180
Db	121	TPHSYIDTYFDTERSSTYRSKGF	DVTVKYTQGSWTG	FGVGEDLV	TIPKGFNTSFLVNIATI 180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDS	SLVTQANIPNVFSMQMCGAGLPVA	240	
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDS	SLVTQANIPNVFSMQMCGAGLPVA	240	
Qy	241	GGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD	CREYNADKA	300	
Db	241	GGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD	CREYNADKA	300	
Qy	301	IVDSGTTLLRLPQKVFD	AVEAVARASLIPEFSDGFWTGS	QLACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLLRLPQKVFD	AVEAVARASLIPEFSDGFWTGS	QLACWTNSETPWSYFPKISI	360
Qy	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420		
Db	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420		
Qy	421	RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480		
Db	421	RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480		
Qy	481	AILLVLIVLLLLPFR	CQRRPRDPEVVNDESSLVRHRWK	518	
Db	481	AILLVLIVLLLLPFR	CQRRPRDPEVVNDESSLVRHRWK	518	

RESULT 8
US-09-978-295A-196
; Sequence 196, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936

; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
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; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
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; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR FILING DATE: 1998-04-15

; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
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; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600

Db 361 YLRDENSRSFRITILPQLYIQPMMGAGLNYECYRF'GISPSTNALVIGATVMEGFYVIED 420

Qy 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
 |||

Db 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

Qy 481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
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Db 481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518

RESULT 9

US-09-886-143-2

; Sequence 2, Application US/09886143
 ; Patent No. US20020159991A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cordell, Barbara
 ; APPLICANT: Schimmoller, Frauke
 ; APPLICANT: Liu, Yu-Wang
 ; APPLICANT: Quon, Diana Hom
 ; TITLE OF INVENTION: Modulation of A Levels by
 ; TITLE OF INVENTION: Secretase BACE2
 ; FILE REFERENCE: SCIOS.022A
 ; CURRENT APPLICATION NUMBER: US/09/886,143
 ; CURRENT FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 60/215,729
 ; PRIOR FILING DATE: 2000-06-28
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 518
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-886-143-2

Query Match 100.0%; Score 2687; DB 9; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2.8e-240;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60
 |||

Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60

Qy 61 ALALEPALASPAGAAFLAMVDNLQGD SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
 |||

Db 61 ALALEPALASPAGAAFLAMVDNLQGD SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy 121 TPHSYIDTYFDTERSSTYRSKGFDVT VKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
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Db 121 TPHSYIDTYFDTERSSTYRSKGFDVT VKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180

Qy 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
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Db 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy 241 GSGTNGGSLVLGGIEPSLYKGD IWTPIKEEWYQIEILKLEIGGQSLNLD CREYNADKA 300
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Db 241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
 Qy 301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
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 Db 301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
 Qy 361 YLRDENSSRSFRITILPQLYIQPMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
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 Db 361 YLRDENSSRSFRITILPQLYIQPMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
 Qy 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
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 Db 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
 Qy 481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
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RESULT 10

US-09-978-697-196

; Sequence 196, Application US/09978697

; Patent No. US20020169284A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C27

; CURRENT APPLICATION NUMBER: US/09/978,697

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match          100.0%;  Score 2687;  DB 9;  Length 518;
Best Local Similarity 100.0%;  Pred. No. 2.8e-240;
Matches 518;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy          1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPATPAERHADGL 60
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Db 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPPTPAERHADGL 60

Qy 61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
 |||

Db 61 ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
 |||

Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180

Qy 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVA 240
 |||

Db 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVA 240

Qy 241 GSGTNGGSLVLGGIEPSLYKGGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300
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Db 241 GSGTNGGSLVLGGIEPSLYKGGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300

Qy 301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
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Db 301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360

Qy 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
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Db 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy 421 RAQKRVGFAASPCAIEIAGAASVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCG 480
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Db 421 RAQKRVGFAASPCAIEIAGAASVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCG 480

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Db 481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518

RESULT 11

US-09-978-192A-196

; Sequence 196, Application US/09978192A

; Patent No. US20020177553A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
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 ; APPLICANT: Gao, Wei-Qiang
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 ; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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Query Match 100.0%; Score 2687; DB 9; Length 518;
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Db	121	TPHSYIDTYFDTERSSTYRSKGF	DVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
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Qy	301	IVDSGTLLRLPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ	LACWTNSETPWSYFPKISI 360
Db	301	IVDSGTLLRLPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ	LACWTNSETPWSYFPKISI 360
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Db	361	YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD		420
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Db	421	RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG		480
Qy	481	AILLVLIVLLLLPFR	CQRRPRDPEVVNDESSLVRHRWK	518
Db	481	AILLVLIVLLLLPFR	CQRRPRDPEVVNDESSLVRHRWK	518

RESULT 12

US-09-999-832A-196

; Sequence 196, Application US/09999832A

; Publication No. US20020192706A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
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; CURRENT FILING DATE: 2001-10-24
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
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Best Local Similarity 100.0%; Pred. No. 2.8e-240;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPCTPAERHADGL 60

Qy     61 ALALEPALASPAGAAFLAMVDNIQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
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Db     61 ALALEPALASPAGAAFLAMVDNIQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy    121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGFNTSFLVNIATI 180
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Db    121 TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVITIPKGFNTSFLVNIATI 180

Qy    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
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Db    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy    241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300
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Db    241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300

Qy    301 IVDSGTTLRLRPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
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Db    361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
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Qy 421 RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
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 Qy 481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
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RESULT 13

US-09-978-189-196

; Sequence 196, Application US/09978189

; Publication No. US20030004102A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
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 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C7

; CURRENT APPLICATION NUMBER: US/09/978,189

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1997-11-13

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; PRIOR APPLICATION NUMBER: 60/085697

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Db    121 TPHSYIDTYFDTERSSTYRSKGFDVT VKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180

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Db	241	GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Qy	361	YLRDENSSRSFRITILPQLYIQPMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Db	361	YLRDENSSRSFRITILPQLYIQPMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Qy	421	RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480
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Qy	481	AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK	518
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RESULT 14

US-09-978-608A-196

; Sequence 196, Application US/09978608A

; Publication No. US20030045462A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
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 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
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 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey

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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 196
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-978-608A-196
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Query Match          100.0%; Score 2687; DB 10; Length 518;
Best Local Similarity 100.0%; Pred. No. 2.8e-240;
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGL 60

Qy     61 ALALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ALALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVITIPKGFNTSFLVNIATI 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVITIPKGFNTSFLVNIATI 180

Qy    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240

Qy    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300

Qy    301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360

Qy    361 YLRDENSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 YLRDENSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420

Qy    421 RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480

Qy    481 AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK 518
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK 518
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; Sequence 196, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 196
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-978-585A-196

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Query Match          100.0%;  Score 2687;  DB 10;  Length 518;
Best Local Similarity 100.0%;  Pred. No. 2.8e-240;
Matches 518;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGL 60
|
Db      1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGL 60

Qy     61 ALALEPALASPAGAAANFLAMVDNLQGDSSRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
|
Db     61 ALALEPALASPAGAAANFLAMVDNLQGDSSRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120

Qy    121 TPHSYIDTYFDTERSSTYRSKGFVDTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATI 180
|

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Db 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATI 180
 Qy 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
 Qy 241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA 300
 Qy 301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 IVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
 Qy 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIED 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIED 420
 Qy 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
 Qy 481 AILLVLIVLLLLPFR CQRRPRDPEVVNDESSLVRHRWK 518
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 481 AILLVLIVLLLLPFR CQRRPRDPEVVNDESSLVRHRWK 518

Search completed: February 28, 2004, 09:20:27
 Job time : 36.6364 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2004, 09:05:50 ; Search time 18.5 Seconds
(without alignments)
2693.363 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALARALLPLIAQWLLRA.....RPRDPEVVNDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	1178.5	43.9		501	2	A59090	aspartic proteinas
2	367.5	13.7		383	2	JC7573	pepsinogen C - Afr
3	363.5	13.5		377	1	PEMQCJ	gastricsin (EC 3.4
4	355.5	13.2		384	2	A39314	gastricsin (EC 3.4
5	355	13.2		389	2	JE0371	pepsin C (EC 3.4.2
6	353	13.1		388	2	A29937	gastricsin (EC 3.4
7	351.5	13.1		388	2	JC7246	pepsinogen C - com
8	324.5	12.1		394	2	B43356	gastricsin (EC 3.4
9	320	11.9		385	2	JC7575	pepsinogen A - bul
10	320	11.9		402	1	REMSK	renin (EC 3.4.23.1
11	313.5	11.7		509	2	S66516	oryzasin (EC 3.4.2
12	313	11.6		392	1	A24608	gastricsin (EC 3.4
13	310	11.5		383	2	A41443	pepsin (EC 3.4.23.

14	308.5	11.5	412	1	KHHUD	cathepsin D (EC 3.
15	306.5	11.4	410	1	KHMSD	cathepsin D (EC 3.
16	305.5	11.4	401	1	REMSS	renin (EC 3.4.23.1
17	305	11.4	384	2	JC7574	pepsinogen A - Afr
18	305	11.4	407	1	KHRTD	cathepsin D (EC 3.
19	302	11.2	405	2	A25379	saccharopepsin (EC
20	301.5	11.2	398	2	S66465	cathepsin E (EC 3.
21	300.5	11.2	387	2	C38302	pepsin (EC 3.4.23.
22	299	11.1	398	2	I51185	cathepsin D (EC 3.
23	298.5	11.1	387	2	D38302	pepsin (EC 3.4.23.
24	298.5	11.1	400	2	I47099	renin (EC 3.4.23.1
25	297	11.1	388	1	PEHU	pepsin A (EC 3.4.2
26	296	11.0	388	2	A30142	pepsin A (EC 3.4.2
27	296	11.0	388	2	B30142	pepsin A (EC 3.4.2
28	294.5	11.0	388	1	S19684	pepsin A (EC 3.4.2
29	292	10.9	506	2	T07915	probable aspartic
30	291	10.8	388	1	S19682	pepsin A (EC 3.4.2
31	291	10.8	402	1	RERTK	renin (EC 3.4.23.1
32	291	10.8	406	1	REHUK	renin (EC 3.4.23.1
33	290.5	10.8	396	2	S36865	cathepsin E (EC 3.
34	289	10.8	387	2	E38302	pepsin (EC 3.4.23.
35	288	10.7	387	2	B38302	pepsin (EC 3.4.23.
36	288	10.7	388	1	PEMQAJ	pepsin A (EC 3.4.2
37	287.5	10.7	632	2	T45858	hypothetical prote
38	287	10.7	391	2	A43356	cathepsin E (EC 3.
39	287	10.7	396	2	A34401	cathepsin E (EC 3.
40	286.5	10.7	334	2	JC4870	pepsin A (EC 3.4.2
41	286	10.6	382	1	PECH	pepsin A (EC 3.4.2
42	286	10.6	388	1	PEMQAR	pepsin A (EC 3.4.2
43	285.5	10.6	387	2	JC7245	pepsinogen A - com
44	285	10.6	396	2	T47207	aspartic proteinas
45	284.5	10.6	386	1	PEPG	pepsin A (EC 3.4.2

ALIGNMENTS

RESULT 1

A59090

aspartic proteinase (EC 3.4.23.-) BACE precursor - human

N;Alternate names: beta-secretase; beta-site APP cleaving enzyme

C;Species: Homo sapiens (man)

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 11-May-2000

C;Accession: A59090

R;Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Denis, P.; Teplow, D.B.; Ross, S.; Amarante, P.; Loeloff, R.; Luo, Y.; Fisher, S.; Fuller, J.; Edenson, S.; Lile, J.; Jarosinski, M.A.; Biere, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Treanor, J.; Rogers, G.; Citron, M.

Science 286, 735-741, 1999

A;Title: beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the transmembrane aspartic protease BACE.

A;Reference number: A59090; MUID:20002972; PMID:10531052

A;Note: submitted to GenBank, September 1999

A;Accession: A59090

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-501 <VAS>

A;Cross-references: GB:AF190725; NID:g6118538; PIDN:AAF04142.1; PID:g6118539
 C;Genetics:
 A;Gene: BACE
 C;Superfamily: beta-secretase
 C;Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase; protein digestion; transmembrane protein; zymogen
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-45/Domain: propeptide #status predicted <PRO>
 F;46-501/Product: acid proteinase BACE #status predicted <MAT>
 F;461-477/Domain: transmembrane #status predicted <TRN>
 F;93,289/Active site: Asp #status predicted
 F;153,172,223,354/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;330-380/Disulfide bonds: #status predicted

Query Match 43.9%; Score 1178.5; DB 2; Length 501;
 Best Local Similarity 46.2%; Pred. No. 3.8e-80;
 Matches 240; Conservative 82; Mismatches 164; Indels 33; Gaps 9;

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Qy      7 ALLLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTPGPGTPAERHADGLA 61
      |  || |  |:      : || |      |||      |  |      ||
Db      2 AQALPWLILLWM---GAGVLPAGHTQHGI RLPRLSGLG-----GAPL-----GLR 42

Qy     62 LALE--PALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVA 119
      |  |      |      |: |||||:| ||:||||:| |:||| | |||||
Db     43 LPRETDEEPEEPGRGRGSFVEMVDNLRGKSGQGYVEMTVGSPQTNLILVDTGSSNFAVG 102

Qy    120 GTPHSYIDTYFDTERSSTYRSKGFVDTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIAT 179
      || :: | : : |||||      | | |||| | | : | |||:| | | : |||
Db    103 AAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGWEGELGTDLV SIPHGPNTVRANIAA 162

Qy    180 IFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239
      | ||: ||: | | ||||| ||:| ||| ||||| | ::||:| |:| ||| | :
Db    163 ITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSL VKQTHVPNLFSLQLCGAGFPL 222

Qy    240 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYN 296
      |      : |||::|||: ||| | :|||: ||||: |::|| || | :||:| |
Db    223 NQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYN 282

Qy    297 ADKAIVDSGT'TLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFP 356
      ||:||||| |||:| ||:| |:: || :| |||| | || | |||: ||
Db    283 YDKSIVDSGT'TNLRLPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFP 342

Qy    357 KISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGF 415
      ||:| | | ::||| |||| |::| : : ||:| || | : | :| :|||
Db    343 VISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 402

Qy    416 YVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYAL 475
      ||:||||:| |:| | | : : ||| | | :      | | : :| :
Db    403 YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDDESTLMTIAYVM 462

Qy    476 MSVCGAILLVLLVLLLLPFRQQR--RPRDPEVVNDESSL 512
      ::| | : : : |:: :| | | : : :| | |
Db    463 AAIC-ALFMLPLCLMVCQWRCLRLRQQHDDFADDISLL 500

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pepsinogen C - African clawed frog
 N;Alternate names: progastricsin
 C;Species: *Xenopus laevis* (African clawed frog)
 C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C;Accession: JC7573; PC7118
 R;Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.
 J. Biochem. 129, 147-153, 2001
 A;Title: Amphibian pepsinogens: Purification and characterization of *Xenopus* pepsinogens, and molecular cloning of *Xenopus* and bullfrog pepsinogens.
 A;Reference number: JC7573; MUID:21064922; PMID:11134969
 A;Contents: Stomach
 A;Accession: JC7573
 A;Molecule type: mRNA
 A;Residues: 1-383 <IKU>
 A;Cross-references: DDBJ:AB045379
 A;Accession: PC7118
 A;Molecule type: protein
 A;Residues: 17-68 <IK2>
 C;Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like activity.
 C;Genetics:
 A;Gene: PgC
 C;Superfamily: pepsin
 C;Keywords: stomach; zymogen

Query Match 13.7%; Score 367.5; DB 2; Length 383;
 Best Local Similarity 28.9%; Pred. No. 9.1e-20;
 Matches 132; Conservative 70; Mismatches 154; Indels 101; Gaps 25;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPT	PGPGTPAERHADGL	60
		: :: :: : : :: :		
Db	1	MKFLILALVCLQLSEGIIR----	VPLKKFKFSMREVMRENGIKAPLVDPAT---KYYNQY	52
Qy	61	ALALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120	
		: :: : :		
Db	53	ATAYEP-----LSNYMDM-----	SYIGEISIGTPPQNFLVLFDTGSSNLWVAS	95
Qy	121	TPHSYIDT-----YFDTERSSTYRSKGFDTVKYTGGSWTGFVGEDLVTIPKGENTSF	173	
		: : :: :		
Db	96	T---YCQSQACTNHPLFNPSQSSTYSSNQQFSLQYGTGSLTGILGYDVTVTIQ-----	145	
Qy	174	LVNIATIFESENFFL----PG-----IKWNGILGLAYATLAKPSSSLETFFDSLVTQANI	224	
		: : : : : : :		
Db	146	--NVA--ISQQEFGGLSETEPGTNFVYAQFDGILGLAYPSIAVGGAT--TVMQGM--QQNL	198	
Qy	225	PN--VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLE	282	
		: : : :: : :: : ::		
Db	199	LNQPIFGFYLSGQ-----SSQNGGEVAFGGVDQNYTGTQIYWTPVTSETYWQIGIQGFS	252	
Qy	283	IGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ	342	
		: : : : : :::: : : :		
Db	253	INGQATGW-CSQ--GCQAIVDTGTSLTAPQSVFSSLIQSIG-----AQQDQNGQYV	301	
Qy	343	ACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPOLYI-QPMMGAGLNYECYRFGIS--	399	
		: : : : :		
Db	302	VSCSNIQN----LPTISFTI----SGVSFPLP--PSAYVLQQSSG-----YC-TIGIMPT	345	


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Qy      56 HADGLALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSN 115
      |  |:: ||      :| :|      |: |: ||||| :| |||||
Db      44 HFGDLSVSYEP-----MAYMD-----AAYFGEISIGTPPQNFLVLFDTGSSN 85

Qy     116 FAV-----AGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLV TIPK 167
      |      | | | |      |: | | | : |      ::| | | | | | :| :
Db      86 LWVPSVYCQSQACTSHS---RFNPSESSTYSTNGQTFSLQYSGSLTGFFGYDTLTV-- 139

Qy     168 GFNTSFLVNIATIFESENFLLPG-----IKWNGILGLAYATLAKPSSSLETFFDSLVTQA 222
      | |      | | | |      |::|:|:| | | | | |:: :| :| :
Db     140 ---QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMGLAYPTLSVDGAT--TAMQGMVQEG 192

Qy     223 NIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKL 281
      : : :|: :      |::|:|:| |:: | | | |:: |: :| |::| | :
Db     193 ALTSPIFSVYLSAQ-----QGSSGGAUVFVGVDSSLYTGQIYWAPVTQELYWQIGIEEF 246

Qy     282 EIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQ 341
      |||: | |      :|||:|:| | :|: |::| |::| |::|
Db     247 LIGGQASGW-CSE--GCQAIVDTGTSLTLTPVQQYMSALLQA-----TGAQ 288

Qy     342 LACWTNSETPWSYF-----PKISYLRDENSSRSFRITILPQLYIQPMAGLNY 391
      | : |      | :: :      : | | |      ||
Db     289 -----EDEYGQFLVNCNSIQNLPTLTFFII-----NGVEFPLPPSSYI-----LNN 328

Qy     392 ECY-RFGISP-----STNALVIGATVMEGFYVIFDRAQKRVGFAAS 431
      | | : |      | :| : :| :| : | | | :
Db     329 NGYCTVGVEPTYLSAQNSQPLWILGDVFLRSYYSVYDLSNNRVGFATA 376

```

RESULT 4

A39314

gastricsin (EC 3.4.23.3) precursor - bullfrog

C;Species: *Rana catesbeiana* (bullfrog)

C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 22-Jun-1999

C;Accession: A39314

R;Yakabe, E.; Tanji, M.; Ichinose, M.; Goto, S.; Miki, K.; Kurokawa, K.; Ito, H.; Kageyama, T.; Takahashi, K.

J. Biol. Chem. 266, 22436-22443, 1991

A;Title: Purification, characterization, and amino acid sequences of pepsinogens and pepsins from the esophageal mucosa of bullfrog (*Rana catesbeiana*).

A;Reference number: A39314; MUID:92042186; PMID:1939266

A;Accession: A39314

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-384 <YAK>

A;Cross-references: GB:M73750; NID:g213687; PIDN:AAA49530.1; PID:g213688

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 13.2%; Score 355.5; DB 2; Length 384;

Best Local Similarity 26.5%; Pred. No. 7.2e-19;

Matches 120; Conservative 73; Mismatches 136; Indels 123; Gaps 21;

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Qy      23 ELAPAPFTLPLRVAAATNRVV-----APTPGPGTFAERHADGLALALEPALASPAGAA 76
      :|: :|: : |: | | | | : : : | | | | |
Db      12 QLSEGIKVKPLKKFKSMREVMRDHGKAPVVDPAT---KYNNNEATAFEP-----LAN 61

```



```

Qy      127 DTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTI PKGFN-----TS 172
      ||   |||: ::   ::| || || | ||| :| :   ||
Db      114 --EFDPNESSTFSTQDEFFSLQYSGSLTGIFGFDVTI-QGISITNQEFGLSETEPGTS 170

Qy      173 FLVNIATIFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPN--VFSM 230
      || :   ::||| |||: ::   | :   |   : | | : : |||
Db      171 FLYS-----PFDGILGLAFPSI---SAGGATTVMQKMLQENLLDFPVFSF 212

Qy      231 QMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNL 290
      : |   | : || || |||: ||| | | : || : : | : || |   : |||
Db      213 YLSGQ-----EGSQGGELVFGGVDPNLYTGQITWTPVTQTTYWQIGIEDFAVGGQSSGW 266

Qy      291 DCREYNADKAIVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQ LACWTNSET 350
      | :   : |||: ||| :| : ||   :: :   : |   : | : | : |
Db      267 -CSQ--GCQGIVDTGTSLLTVPNQVFTELMQYIG-----AQADD---SGQYVASCNIE- 314

Qy      351 PWSYFPKI-----SIYLRDENS---SRSFRTILPQLYIQPMMGAGLNIECY 394
      | | |   | | :   || :   | ||   || :
Db      315 ---YMP TITFVISGTSFPLPPSAYMLQSN SDYCTVGIESTYLPSQTGQPLW----- 362

Qy      395 RFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAAS 431
      : : |   : : | | :|   : ||| :
Db      363 -----ILGDVFLRVYYSIYDMGNNQVGFATA 388

```

RESULT 6

A29937

gastricsin (EC 3.4.23.3) precursor - human

N;Alternate names: pepsin C; pepsinogen C

C;Species: Homo sapiens (man)

C;Date: 17-Oct-1988 #sequence_revision 17-Oct-1988 #text_change 31-Mar-2000

C;Accession: A29937; A31811; PX0028; I54213; A91125; A23458

R;Hayano, T.; Sogawa, K.; Ichihara, Y.; Fujii-Kuriyama, Y.; Takahashi, K.

J. Biol. Chem. 263, 1382-1385, 1988

A;Title: Primary structure of human pepsinogen C gene.

A;Reference number: A29937; MUID:88087276; PMID:3335549

A;Accession: A29937

A;Molecule type: DNA

A;Residues: 1-388 <HAY>

R;Taggart, R.T.; Cass, L.G.; Mohandas, T.K.; Derby, P.; Barr, P.J.; Pals, G.; Bell, G.I.

J. Biol. Chem. 264, 375-379, 1989

A;Title: Human pepsinogen C (progastricsin). Isolation of cDNA clones, localization to chromosome 6, and sequence homology with pepsinogen A.

A;Reference number: A31811; MUID:89079679; PMID:2909526

A;Accession: A31811

A;Molecule type: mRNA

A;Residues: 1-388 <TAG>

A;Cross-references: GB:J04443; NID:g551175; PIDN:AAA60074.1; PID:g551176

R;Athauda, S.B.P.; Tanji, M.; Kageyama, T.; Takahashi, K.

J. Biochem. 106, 920-927, 1989

A;Title: A comparative study on the NH2-terminal amino acid sequences and some other properties of six isozymic forms of human pepsinogens and pepsins.

A;Reference number: PX0023; MUID:90130402; PMID:2515193

A;Accession: PX0028

A;Molecule type: protein

A;Residues: 17-101 <ATH>

R;Pals, G.; Azuma, T.; Mohandas, T.K.; Bell, G.I.; Bacon, J.; Samloff, I.M.; Walz, D.A.; Barr, P.J.; Taggart, R.T.
Genomics 4, 137-148, 1989

A;Title: Human pepsinogen C (progastricsin) polymorphism: evidence for a single locus located at 6p21.1-pter.

A;Reference number: I54213; MUID:89290840; PMID:2567697

A;Accession: I54213

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-388 <RES>

A;Cross-references: GB:M23077; NID:g189830; PIDN:AAA60063.1; PID:g387015; GB:J03063

A;Note: parts of this sequence, including the amino end and carboxyl ends of the mature protein, were determined by protein sequencing

R;Foltmann, B.; Jensen, A.L.

Eur. J. Biochem. 128, 63-70, 1982

A;Title: Human progastricsin. Analysis of intermediates during activation into gastricsin and determination of the amino acid sequence of the propeptide.

A;Reference number: A91125; MUID:83079318; PMID:6816595

A;Accession: A91125

A;Molecule type: protein

A;Residues: 17-39, 'ED', 42-51, 'S', 53-64 <FOL>

A;Note: pro-form; 29-Leu was also found

A;Note: activation at pH 2 is proposed to involve conformation change, cleavage after Phe-42, and cleavage after Leu-59

C;Genetics:

A;Gene: GDB:PGC

A;Cross-references: GDB:119485; OMIM:169740

A;Map position: 6p21.3-6p21.1

A;Introns: 20/2; 70/3; 110/1; 149/3; 216/2; 256/2; 305/3; 338/3

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; hydrolase; protein digestion; stomach; zymogen

F;1-16/Domain: signal sequence #status predicted <SIG>

F;17-59/Domain: propeptide #status experimental <PRO>

F;60-388/Product: gastricsin #status experimental <MAT>

Query Match 13.1%; Score 353; DB 2; Length 388;

Best Local Similarity 29.1%; Pred. No. 1.1e-18;

Matches 120; Conservative 65; Mismatches 120; Indels 108; Gaps 21;

```
Qy      52 PAERHADG-LALALEPALASPAGAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVD 110
      || :: | |:: ||                      :| :|          |: |: | | | | | | :| |
Db      50 PAWKYRFGDLSVTYEP-----MAYMD-----AAYFGEISIGTPPQNFLVLFD 91

Qy     111 TGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDL 162
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      92 TGSSNLWVPSVYCQSQACTSHS----RFNPSESSTYSTNGQTFSLQYGSGLTGFFGYDT 147

Qy     163 VTIPKGFNTSFLVNIATIFESENFPLPG-----IKWNGILGLAYATLAKPSSSLETFFDS 217
      :| :|      | |      | | | | | | | | | | | | | | | | | | | | | |
Db     148 LTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMGLAYPALSVDEAT--TAMQG 198

Qy     218 LVTQANIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQI 276
      :| :| :| :| | | | | | | | | | | | | | | | | | | | | | | | |
Db     199 MVQEGALTSPVFSVYLSNQ-----QGSSGGAVVFGGVDSSSLYTGTQIYWAPVTQELYWQI 252

Qy     277 EILKLEIGGQSLNLDREYNADKAIVDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDGF 336
```

```

      | : |||: | | :|||:|:| | :|: |::|
Db      253 GIEEFLIGGQASGW-CSE--GCQAIVDGTGTSLLTVPQQYMSALLQA----- 295

Qy      337 WTGSQLACWTNSETPWSYF-----PKISIIYLRDENSRRSFRITILPOLYIQPMMG 386
      ||:| | : | | : : | |
Db      296 -TGAQ-----EDEYGQFLVNCNSIQNLPSLTFII-----NGVEFPLPPSSYI----- 336

Qy      387 AGLNYECY-RFGISP----STNA---LVIGATVMEGFYVIFDRAQKRVGFAAS 431
      |: | |: | | | :| : | :| | | | :
Db      337 --LSNNGYCTVGVEPTYLSSQNGQPLWILGDVFLRSYYSVYDLGNNRVGFATA 387

```

RESULT 7

JC7246

pepsinogen C - common marmoset

C;Species: Callithrix jacchus (common marmoset)

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000

C;Accession: JC7246

R;Kageyama, T.

J. Biochem. 127, 761-770, 2000

A;Title: New world monkey pepsinogens A and C, and prochymosins. Purification, characterization of enzymatic properties, cDNA cloning, and molecular evolution.

A;Reference number: JC7245

A;Accession: JC7246

A;Molecule type: mRNA

A;Residues: 1-388 <KAG>

A;Cross-references: DDBJ:AB038385

A;Experimental source: strain NW791

C;Comment: This protein, a zymogen of pepsins, is the major proteolytic enzyme in vertebrate gastric juices. It plays roles in gastric digestion, and is a useful molecular marker for clarifying the evolution of mammalian orders and families.

C;Superfamily: pepsin

C;Keywords: gastric juice; zymogen

```

Query Match          13.1%; Score 351.5; DB 2; Length 388;
Best Local Similarity 30.1%; Pred. No. 1.4e-18;
Matches 112; Conservative 56; Mismatches 115; Indels 89; Gaps 17;

```

```

Qy      92 YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGF 143
      |: |: ||||| :| ||||| | | | | | | | | | | |
Db      73 YFGEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHS----RFNPSASSTYSSNGQ 128

Qy      144 DVTVKYTQGSWTGFVGEDLV TIPKGFNTSFLVNIATIFESENFFLPG-----IKWNGILG 198
      :::| || ||| | | :|: | | | | | | | | | | |
Db      129 TFSLQYGSGLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG 181

Qy      199 LAYATLAKPSSSLETFFDSLVTQANIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPS 257
      ||| |: : : | : : : : | | | | | | | | | | |
Db      182 LAYPALSMGGAT--TAMQGMLEQEGALTSPVFSFYLSNQ-----QGSSGGAVIFGGVDSS 233

Qy      258 LYKGDIIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFD 317
      || | |:| |: :| |:| | : | | | : | | | | | | |
Db      234 LYTGQIIYWAPVTQELYWQIGIEEFLIGGQASGW-CSE--GCQAIVDGTGTSLLTVPQQYMS 290

Qy      318 AVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYF-----PKISIIYLRDENS 367
      | :|| | | | | | | | | | | | | | | | |

```

```

Db      291 AFLEA-----TGAQ-----EDEYGQFLVNCDSIQNLPTLTFII----- 323
Qy      368 SRSFRITILPQLYIQPMMGAGLNYECY-RFGISP-----STNALVIGATVMEGFYVIF 419
          : | ||      | : | | : |      | : | : | : |
Db      324 -NGVEFPLPPSSYI-----LSNNGYCTVGVEPTYLSSQNSQPLWILGDVFLRSYYSVF 375
Qy      420 DRAQKRVGFAAS 431
          | |||| :
Db      376 DLGNNRVGFATA 387

```

RESULT 8

B43356

gastricsin (EC 3.4.23.3) precursor - guinea pig

N;Alternate names: pepsin C

C;Species: Cavia porcellus (guinea pig)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999

C;Accession: B43356

R;Kageyama, T.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Koiwai, O.;

Tanji, M.; Yakabe, E.; Athauda, S.B.; Takahashi, K.

J. Biol. Chem. 267, 16450-16459, 1992

A;Title: Gastric procathepsin E and progastricsin from guinea pig. Purification, molecular cloning of cDNAs, and characterization of enzymatic properties, with special reference to procathepsin E.

A;Reference number: A43356; MUID:92355614; PMID:1644829

A;Accession: B43356

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-394 <KAG>

A;Cross-references: GB:M88652; NID:g191296; PIDN:AAA37053.1; PID:g191297

A;Note: sequence extracted from NCBI backbone (NCBIN:110805, NCBIP:110806)

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach

```

Query Match          12.1%; Score 324.5; DB 2; Length 394;
Best Local Similarity 29.0%; Pred. No. 1.5e-16;
Matches 107; Conservative 63; Mismatches 116; Indels 83; Gaps 18;

```

```

Qy      92 YYLEMLIGTPPQKLQILVDTGSSNF-----AVAGTPHSYIDTYFDTERSSTYRSKGF 143
          | : :: : |||| | : | |||| |      : : | | | : | || | :
Db      79 YFGQISLGTTPPQSFQVLFDTGSSNLWVPSVYCSSLACTTH----TRFNPRDSSTYVATDQ 134
Qy      144 DVTVKYTQGSWTGFVGEDLVTI-----PK-GFNTSFLVNIATIFESENFFLPG-----IK 192
          : :: | || || | | : || | | | | | : | | | :
Db      135 SFSLEYGTGSLTGFGYDTMTIQDIQVPKQEFGLS-----ETE----PGSDFVYAE 181
Qy      193 WNGILGLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGS--GTNGGSL 249
          : : |||| | | : : : | : : : : || : : | | : | |
Db      182 FDGILGLGYPGLSEGGAT--TAMQGLLREGALSQSLFSVYL-----GSQQGSDEGQL 231
Qy      250 VLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLL 309
          : ||| : : || | || : || : | | : | | : | | : || : ||
Db      232 ILGGVDESLYTGDIYWTPTQELYWQIGIEGLIDGSASGWCSR---GCQGIVDTGTSLL 288
Qy      310 RLPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSSR 369
          : | : : : | : : | : : | : : | :

```

```

Db      289 TVPSDYSLTLVQAIGAE--NEYGEYF-----VSCSSIQLPTLTLFVISGV----- 332
Qy      370 SFRITILPQLYIQP-----MMGAGLNYECYRFGISPSTN--ALVIGATVMEGFYVIFDRA 422
          : | ||      |:|  |      :||      ::|  :  :| :| |
Db      333 --EFPLSPSAYILSGENYCMVGLESTY-----VSPGGGEPVWILGDVFLRSYYSVYDLA 384
Qy      423 QKRVGFAAS 431
          ||||| :
Db      385 NNRVGFATA 393

```

RESULT 9

JC7575

pepsinogen A - bullfrog

C;Species: *Rana catesbeiana* (bullfrog)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001

C;Accession: JC7575

R;Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasu, S.

J. Biochem. 129, 147-153, 2001

A;Title: Amphibian pepsinogens: Purification and characterization of *Xenopus* pepsinogens, and molecular cloning of *Xenopus* and bullfrog pepsinogens.

A;Reference number: JC7573; MUID:21064922; PMID:11134969

A;Contents: Stomach

A;Accession: JC7575

A;Molecule type: mRNA

A;Residues: 1-385 <IKU>

A;Cross-references: DDBJ:AB045376

C;Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like activity.

C;Genetics:

A;Gene: PgA

C;Superfamily: pepsin

C;Keywords: stomach; zymogen

```

Query Match          11.9%; Score 320; DB 2; Length 385;
Best Local Similarity 27.8%; Pred. No. 3.2e-16;
Matches 111; Conservative 67; Mismatches 147; Indels 74; Gaps 15;

```

```

Qy      50 GTPAERHADGLALALEPALASPAGAAANFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILV 109
          |  ::|  |  |::|  :|  : ||  | : | ||||  ::
Db      39 GDYLKKHHYNPATKYFPSLAQASG-----EPLQNYMDIEYFGTISIGTPPQSFTVIF 90
Qy      110 DTGSSNFAVAGTPHSYIDT-----YFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDL 162
          |||||  |  |  | :  | : ::|||::  |::|  || :||:|  |
Db      91 DTGSSNLWV---PSVYCSPACTNHHMFNPQQSSSTFQATNTPVSIQYGTGSMGFLGYDT 147
Qy      163 VTIPKGFNTSFLVNIATIFESE-NFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQ 221
          | :  |  | : :||  ||  : ||||| : :||  ||  ||::  |
Db      148 VQVG---NIQITNQIFGLSQSEPGSFLYSPFDGILGLAFPSLA--SSQATPVFDNMWNQ 202
Qy      222 ANIP-NVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILK 280
          || :||: :  :  | :|  :: ||:|  || |:: : | : | ||:  |
Db      203 GLIPQDLFSVYL-----SSQGQSGSFVLFGGVDTSYYTGNLNWVPLTAETYWQITVDS 255
Qy      281 LEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGS 340
          : |||| :  :  ||||:|:|  |  | : :  | :  : | :| :
Db      256 ISIGGQVIACS----GSCSAIVDTGTSLLAGPSTPI-ANIQQYIGAN---QDSNGQYV-- 305

```

```

QY      341 QLACWTNSETPWSYFP-----KISIIYLRDENSS--RSFRITILPQLYIQPMMGAGLN 390
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      306 -INCNNISNMPTVVFTINGVQYPLPASAYVRQSQQSCTSGFQAMNLP----- 351

QY      391 YECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFA 429
      : | : ::| : : ||:|||| | | |
Db      352 -----TSSGDLWLIGDVFIREYYVVFDRANNYVAMA 382

```

RESULT 10

REMSK

renin (EC 3.4.23.15) precursor, renal - mouse

N;Alternate names: angiotensin-forming enzyme; angiotensinogenase; renin 1

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999

C;Accession: A00989; S07636; A22766; A22058; I57576; A05137; JH0083

R;Holm, I.; Ollo, R.; Panthier, J.J.; Rougeon, F.

EMBO J. 3, 557-562, 1984

A;Title: Evolution of aspartyl proteases by gene duplication: the mouse renin gene is organized in two homologous clusters of four exons.

A;Reference number: A00989; MUID:84182525; PMID:6370686

A;Accession: A00989

A;Molecule type: DNA

A;Residues: 1-402 <HOL>

A;Cross-references: EMBL:X00850

R;Kim, W.S.; Murakami, K.; Nakayama, K.

Nucleic Acids Res. 17, 9480, 1989

A;Title: Nucleotide sequence of a cDNA coding for mouse Ren1 preprorenin.

A;Reference number: S07636; MUID:90067953; PMID:2685761

A;Accession: S07636

A;Molecule type: mRNA

A;Residues: 1-402 <KIM>

A;Cross-references: EMBL:X16642; NID:g53930; PIDN:CAA34636.1; PID:g53931

R;Mullins, J.J.; Burt, D.W.; Windass, J.D.; McTurk, P.; George, H.; Brammar, W.J.

EMBO J. 1, 1461-1466, 1982

A;Title: Molecular cloning of two distinct renin genes from the DBA/2 mouse.

A;Reference number: A90968; MUID:84207899; PMID:6327270

A;Accession: A22766

A;Molecule type: mRNA

A;Residues: 269-314,'D',316 <MUL>

R;Panthier, J.J.; Dreyfus, M.; Roux, D.T.L.; Rougeon, F.

Proc. Natl. Acad. Sci. U.S.A. 81, 5489-5493, 1984

A;Title: Mouse kidney and submaxillary gland renin genes differ in their 5' putative regulatory sequences.

A;Reference number: A22058; MUID:84298161; PMID:6089205

A;Accession: A22058

A;Molecule type: DNA

A;Residues: 1-30 <PAN>

R;Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W.

Mol. Cell. Biol. 4, 2321-2331, 1984

A;Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analysis of 5'-proximal flanking regions.

A;Reference number: I57576; MUID:85085936; PMID:6392850

A;Accession: I57576

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-31 <RES>

A;Cross-references: GB:K02800; NID:g200689; PIDN:AAA40044.1; PID:g200690

C;Comment: The only known function of renal renin is to release angiotensin I from angiotensinogen in the plasma, initiating a cascade of reactions that produces an elevation of blood pressure and increased sodium retention by the kidney.

C;Comment: Renal renin is synthesized by the juxtaglomerular cells of the kidney in response to decreased blood pressure and sodium concentration.

C;Genetics:

A;Gene: Ren-1

A;Introns: 31/2; 81/3; 123/1; 162/3; 228/2; 268/2; 316/3; 349/3

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; blood pressure control; glycoprotein; hydrolase; kidney; plasma

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-64/Domain: propeptide #status predicted <PRO>

F;65-402/Product: renin #status predicted <MAT>

F;69,139,320/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;102,287/Active site: Asp #status predicted

Query Match 11.9%; Score 320; DB 1; Length 402;

Best Local Similarity 28.6%; Pred. No. 3.4e-16;

Matches 126; Conservative 66; Mismatches 181; Indels 68; Gaps 21;

```
Qy      10 LPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPG-PGTPAERHADGLALALE--- 65
          :|| | ||      :| |:|| ||      : |      || | | : |
Db       6 MPLWALLLL-----WSPCTFSLPTRTATFERIPLKKMPSVREILEERGVDMLRLSAEWGV 60

Qy      66 ----PA---LASPAGAAFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAV 118
          | : | || | :| | | || | : ||||| : : ||||:| |
Db      61 FTKRPSLTNLTSPVVLTNYL-----NTQ-----YYGEIGIGTPPQTFKVFIDTGSANLWV 110

Qy     119 AGTPHSY-----IDTYFDTERSSTYRSKGFDTVVKYTOGSWTGFVGEDLVITPKGFNTS 172
          | |      | : : : ||:| | | | : | | ||: :| ||: | :
Db     111 PSTKCSRLYLACGIHSLYESSDSSSYMENGSDFTIHYGSGRVKGFSLQDSVTV-GGITVT 169

Qy     173 FLVNIATIFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQ 231
          | |      | | | :||:| : | : | : || : :| : ||:
Db     170 QTFGEVTELPLIPFML--AKFDGVLGMGFP--AQAVGGVTPVFDHILSQGVLKKEEVFSVY 225

Qy     232 MCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD 291
          ||      || :||| :| | :| : | | : :|| : : :| | |
Db     226 Y-----NRGSHLLGGEVVLGGSDPQHYQGNFHYVSISKTPSQITMKGVSVG--SSTLL 277

Qy     292 CREYNADKAIVDSGTTLLRLPQKVFDVAVVEAV-ARASLIPEFSDGFWTGSQACWTNSET 350
          | | | :||:| : : | : :||:| : | | : : | | :
Db     278 CEEGCA--VVVDTGSSSFISAPTSSLKLIMQALGAKEKRIEY-----VVNC---SQV 324

Qy     351 PWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMAGL-NYECYRFGISPSTNAL-VIG 408
          | | | || | | | : : : : | | | : | | | : | :|
Db     325 P--TLPDISFDL----GGRAYTLSSTDYVLQYPNRRDKLCTLALHAMDIPPTGPVWVLG 378

Qy     409 ATVMEGFYVIFDRAQKRVGFA 429
          || : || || | :|||
Db     379 ATFIRKFYTEFDRHNNRIGFA 399
```

RESULT 11

S66516

oryzasin (EC 3.4.23.-) precursor - rice

N;Alternate names: aspartic proteinase 1

C;Species: Oryza sativa (rice)

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C;Accession: S66516; S66517

R;Asakura, T.; Watanabe, H.; Abe, K.; Arai, S.

Eur. J. Biochem. 232, 77-83, 1995

A;Title: Rice aspartic proteinase, oryzasin, expressed during seed ripening and germination, has a gene organization distinct from those of animal and microbial aspartic proteinases.

A;Reference number: S66516; MUID:96048031; PMID:7556174

A;Accession: S66516

A;Molecule type: DNA

A;Residues: 1-509 <ASA>

A;Cross-references: EMBL:D32165; NID:g511665; PIDN:BAA06876.1; PID:g1030715

A;Accession: S66517

A;Molecule type: mRNA

A;Residues: 1-509 <ASZ>

A;Cross-references: EMBL:D32144; NID:g1255684; PIDN:BAA06875.1; PID:g1711289

C;Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 represent a cyclical permutation of a single saposin repeat.

C;Genetics:

A;Introns: 119/3; 140/1; 171/3; 209/2; 265/3; 279/1; 300/3; 338/3; 360/2; 412/3; 452/3; 482/2

C;Superfamily: oryzasin; saposin repeat homology

C;Keywords: aspartic proteinase; hydrolase

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-68/Domain: propeptide #status predicted <PRO>

F;68-509/Product: aspartic proteinase 1 #status predicted <MAT>

F;316-361/Domain: saposin repeat homology #status atypical <SAP1>

F;370-420/Domain: saposin repeat homology #status atypical <SAP2>

F;103,290/Active site: Asp #status predicted

Query Match 11.7%; Score 313.5; DB 2; Length 509;

Best Local Similarity 23.0%; Pred. No. 1.5e-15;

Matches 127; Conservative 75; Mismatches 179; Indels 171; Gaps 19;

```

Qy      3 ALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGLAL 62
      ::|  ||  :|  ||  ||  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      5 SVALVLLAAVLLQALLPASAEGLVRIALKRPIDENS RVAARLSG-----EEGARRLGL 59

Qy     63 ALEPALASPAGAAFLAMVDNLQGD SGRGYYLEMLIGTPPQKLQILVDTGSSN----- 115
      :|  |  |  :  ::  :  :  |  |  |  :  |||||  :  |||||
Db     60 RGANSLGGGGGEGDIVALKNYMNAQ----YFGEIGVGTTPPQKFTVIFDTGSSNLWVPSAK 115

Qy    116 --FAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSF 173
      |::|  ||  :  :  :|||:  |  :  :|  ||  ||  ||  ||:
Db    116 CYFSIACFFHS----RYKSGQSSTYQKNGKPAAIQYGTGSIAGFFSEDSVTVGD----- 165

Qy    174 LVNIATIFESENEFF----LPGI-----KWNIGILGLAYATLAKPSSSLETFFDSLVTQANI 224
      :  :  :  |  ||:  |::|||  :  ::  :  :
Db    166 -----LVVKDQEFIEATKEPGLTFMVAKFDGILGLGFQEISVGDA-----V 206

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Qy 225 PNVFSMQMCG-AGLPVAGSGTN-----GGSLVLGGIEPSLYKGDIWYTPIKEEWYYQI 276
 | : | | | | | | | | : | | : | | | : | | : : | : |
 Db 207 PVWYKMVEQGLVSEPVSFVFNHRSDEGEGGEIVFGMDPSHYKGNHTYVPVSQKGYWQF 266

 Qy 277 EILKLEIGGQSLNLDCREYNADKAIVDSGTLLRLPQKVFDVAVEAVARASLIPE----- 331
 | : : | | : | : | | | | : | : : | : : :
 Db 267 EMGDVLIGGKTTGF-CA--SGCSAIADSGTSLLAGPTAIITEINEKIGATGVVVSQECKTV 323

 Qy 332 -----FSDGF----- 336
 | : |
 Db 324 VSQYGQQILDLLLAETQPSKICSQVGLCTFDGKHGVSAGIKSVVDDEAGESNGLQSGPMC 383

 Qy 337 -----WTGSQLACWTNSETPSY-----FPKISIIYLRD 364
 | : | | : : | | | : | : | :
 Db 384 NACEMAVVWMQNQLAQNKTDLILNYINQLCDKLPSPMGESSVDCGSLASMPEISFTIGA 443

 Qy 365 ENSSRSFRITILPQLYIQPMMGAGLNYECY----RFGISPSTNAL-VIGATVMEGFYVIF 419
 : : : | : | : | : | : | : | : : | : : : |
 Db 444 K-----KFALKPEEYIL-KVGEGAAQCSIGFTAMDIPPPRGPLWILGDVFMGAYHTVF 496

 Qy 420 DRAQKRVGFAAS 431
 | : | | | | |
 Db 497 DYGKMRVGFSAKS 508

RESULT 12

A24608

gastricsin (EC 3.4.23.3) precursor - rat

N;Alternate names: pepsinogen C

N;Contains: pepsin A (EC 3.4.23.1) precursor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1988 #sequence_revision 05-Aug-1994 #text_change 18-Jun-1999

C;Accession: A33510; A24608; C22434; A05145; A61298

R;Ishihara, T.; Ichihara, Y.; Hayano, T.; Katsura, I.; Sogawa, K.; Fujii-Kuriyama, Y.; Takahashi, K.

J. Biol. Chem. 264, 10193-10199, 1989

A;Title: Primary structure and transcriptional regulation of rat pepsinogen C gene.

A;Reference number: A33510; MUID:89255508; PMID:2722863

A;Accession: A33510

A;Molecule type: DNA

A;Residues: 1-392 <ISH>

A;Cross-references: GB:M25985

R;Ichihara, Y.; Sogawa, K.; Morohashi, K.; Fujii-Kuriyama, Y.; Takahashi, K.
Eur. J. Biochem. 161, 7-12, 1986

A;Title: Nucleotide sequence of a nearly full-length cDNA coding for pepsinogen of rat gastric mucosa.

A;Reference number: A24608; MUID:87054020; PMID:3780741

A;Accession: A24608

A;Molecule type: mRNA

A;Residues: 1-392 <ICH>

A;Cross-references: GB:X04644; NID:g56880; PIDN:CAA28305.1; PID:g56881

R;Ichihara, Y.; Sogawa, K.; Takahashi, K.

J. Biochem. 98, 483-492, 1985

A;Title: Isolation of human, swine, and rat prepepsinogens and calf preprochymosin, and determination of the primary structures of their NH2-terminal signal sequences.

A;Reference number: A22434; MUID:86059312; PMID:2415509
A;Accession: C22434
A;Molecule type: protein
A;Residues: 1-19,'X',21-23,'X',25-29 <IC2>
R;Arai, K.M.; Muto, N.; Tani, S.; Akahane, K.
Biochim. Biophys. Acta 788, 256-261, 1984
A;Title: The N-terminal sequence of rat pepsinogen.
A;Reference number: A05145; MUID:84257697; PMID:6743670
A;Accession: A05145
A;Molecule type: protein
A;Residues: 17-30,'Q',32-102,'A',104-108,'L',110-112 <ARA>
A;Experimental source: Wistar strain
R;Ichihara, Y.; Sogawa, K.; Takahashi, K.
J. Biochem. 92, 603-606, 1982
A;Title: Rat gastric prepepsinogen: in vitro synthesis and partial amino-terminal signal sequence.
A;Reference number: A61298; MUID:83030750; PMID:6182139
A;Accession: A61298
A;Molecule type: protein
A;Residues: 1,'XX',4-6,'X',8-9,'X',11,'X',13-14,'XXX',18-19,'X',21,'X',23,'XX',26,'X' <IC3>
C;Comment: This enzyme has more restricted specificity than pepsin A. It is the major form of pepsinogen in rat gastric mucosa.
C;Genetics:
A;Introns: 20/2; 73/3; 113/1; 152/3; 219/2; 259/2; 309/3; 342/3
A;Note: there are at least two very similar genes for gastricsin in rat
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach
F;1-16/Domain: signal sequence #status experimental <SIG>
F;17-392/Product: pepsinogen #status experimental <MAT>
F;17-62/Domain: activation peptide #status experimental <ACT>
F;94,280/Active site: Asp #status predicted
F;107-112,270-275,314-347/Disulfide bonds: #status predicted

Query Match 11.6%; Score 313; DB 1; Length 392;
Best Local Similarity 29.5%; Pred. No. 1.1e-15;
Matches 105; Conservative 56; Mismatches 139; Indels 56; Gaps 16;

```

Qy      92 YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGF 143
      |: |: | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      76 YFGEISIGTPPQNFLVLFDTGSSNLWVSSVYCQSEACTTHA----RFNPSKSSTYYTEGQ 131

Qy     144 DVTVKYTGQSWTGFVGEDLVITPKGFNTSFLVNIATIFESENFFLPG-----IKWNGILG 198
      :::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db     132 TFSLQYGTGSLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG 184

Qy     199 LAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS--GTNGGSLVLGGIEP 256
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     185 LAYPGLS--SGGATTALQGMLGE----GALSQPLFGVYL---GSQQGSNGGQIVFGGVDK 235

Qy     257 SLYKGDIIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLRLPQKVF 316
      : | | | | | | | | | | | | | | | | | | | | | | | | |
Db     236 NLYTGEITWVPVTQELYWQITIDDFLIGDQASGW-CSSQGC-QGIVDTGTSLLVMPAQYL 293

Qy     317 DAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENSSRSFRITIL 376
      ::: : | : : | : : | : : | : : | : : | : : | : :

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Db      294 SELLQTIGAQE--GEYGEYF-----VSCDSVSS-----LPTLSFVL-----NGVQFPLS 335
Qy      377 PQLY-IQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAAS 431
      | | | | : | : | : | | | : | | |
Db      336 PSSYIIQEDNFCMVGLESISLTSESGQPLWILGDVFLRSYYAIFDMGNKVKGLATS 391

```

RESULT 13

A41443

pepsin (EC 3.4.23.-) precursor, embryonic - chicken

C;Species: Gallus gallus (chicken)

C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 21-Jul-2000

C;Accession: A41443

R;Hayashi, K.; Agata, K.; Mochii, M.; Yasugi, S.; Eguchi, G.; Mizuno, T.
J. Biochem. 103, 290-296, 1988

A;Title: Molecular cloning and the nucleotide sequence of cDNA for embryonic
chicken pepsinogen: phylogenetic relationship with prochymosin.

A;Reference number: A41443; MUID:88227903; PMID:3131317

A;Accession: A41443

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-383 <HAY>

A;Cross-references: GB:D00215; NID:g2760810; PIDN:BAA00153.1; PID:g222853

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; hydrolase; protein digestion

```

Query Match          11.5%; Score 310; DB 2; Length 383;
Best Local Similarity 26.8%; Pred. No. 1.8e-15;
Matches 106; Conservative 63; Mismatches 136; Indels 90; Gaps 15;

```

```

Qy      56 HA--DGLALALEPALASPAGAAFLAMVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGS 113
      || | | : || | | | | | | | : || || | : || ||
Db      55 HAFPDVLTVVTEPLL-----NTLDM-----EYYGTISIGTPPQDFTVVFDTG 97

Qy      114 SNFAVAG----TPHSYIDTYFDTERSSSTYRSKGFDTVYKYTQGSWTGFVGEDLV TIPKG 169
      || | : | : | : | : | : | : | : | : | : | : | :
Db      98 SNLWVPVSCTSPACQSHQMFNPSQSSTYKSTGQNL SIHYGTGDMEGTVGCDT VTVASLM 157

Qy      170 NTSFLVNIATIFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI-PNVF 228
      : | : | : | : | : | : | : | : | : | : | : | : | :
Db      158 DTNQLFGLST-SEPGQFFV-YVKFDGILGLGYPSLA--ADGITPVFDNMVNESLLEQNLF 213

Qy      229 SMQMCAGLPVAGSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSL 288
      | : : : | : | | | : | : | : | : | : | : | : | :
Db      214 SVYLSREPM-----GSMVVFEGGIDESYFTGSINWIPVSYQGYWQISMDSIIVNKQEI 265

Qy      289 NLDCREYNADKAI VDSGTTLLRLPQKVFD AVVEAVARASLIPEFSDGFWTGSQLACWTNS 348
      : : | : | : | : | : | : | : | : | : | : | : |
Db      266 ACS----SGCQAIIDTGTSLVAGPASDINDIQSAVG-----ANQ 300

Qy      349 ETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNY-----ECY 394
      | | | | | | | | : | : : | : | : | : | : |
Db      301 NTYGEY-----SVNCSHILAMPDVVF--VIG-GIQYPVPALAYTEQNGQGTCM 345

Qy      395 RFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFA 429
      : | : : | : : | | | | | | | |
Db      346 SSFQNSSADLWILGDVFIRVYYSIFDRANNRVGLA 380

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RESULT 14

KHHUD

cathepsin D (EC 3.4.23.5) precursor [validated] - human

N;Alternate names: preprocathepsin D

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 15-Sep-2000

C;Accession: A25771; S30749; PC2066; I59236; I57716

R;Faust, P.L.; Kornfeld, S.; Chirgwin, J.M.

Proc. Natl. Acad. Sci. U.S.A. 82, 4910-4914, 1985

A;Title: Cloning and sequence analysis of cDNA for human cathepsin D.

A;Reference number: A25771; MUID:85270436; PMID:3927292

A;Accession: A25771

A;Molecule type: mRNA

A;Residues: 1-412 <FAU>

A;Cross-references: EMBL:M11233; NID:g181179; PIDN:AAB59529.1; PID:g181180

R;Westley, B.R.; May, F.E.B.

Nucleic Acids Res. 15, 3773-3786, 1987

A;Title: Oestrogen regulates cathepsin D mRNA levels in oestrogen responsive human breast cancer cells.

A;Reference number: S30749; MUID:87231068; PMID:3588310

A;Accession: S30749

A;Molecule type: mRNA

A;Residues: 1-412 <WES>

A;Cross-references: EMBL:X05344; NID:g29677; PIDN:CAA28955.1; PID:g29678

R;May, F.E.B.; Smith, D.J.; Westley, B.R.

Gene 134, 277-282, 1993

A;Title: The human cathepsin D-encoding gene is transcribed from an estrogen-regulated and a constitutive start point.

A;Reference number: PC2066; MUID:94085791; PMID:8262386

A;Accession: PC2066

A;Molecule type: DNA

A;Residues: 1-23 <MAY>

A;Cross-references: GB:L12980; NID:g291930; PIDN:AAA16314.1; PID:g455429

A;Experimental source: MCF-7 cell

R;Cavaillès, V.; Augereau, P.; Rochefort, H.

Proc. Natl. Acad. Sci. U.S.A. 90, 203-207, 1993

A;Title: Cathepsin D gene is controlled by a mixed promoter, and estrogens stimulate only TATA-dependent transcription in breast cancer cells.

A;Reference number: I59236; MUID:93126342; PMID:8419924

A;Accession: I59236

A;Status: translation not shown; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-22 <CAV1>

A;Cross-references: GB:S52557; NID:g263124; PIDN:AAD13868.1; PID:g4261568

R;Augereau, P.; Miralles, F.; Cavaillès, V.; Gaudelot, C.; Parker, M.; Rochefort, H.

Mol. Endocrinol. 8, 693-703, 1994

A;Title: Characterization of the proximal estrogen-responsive element of human cathepsin D gene.

A;Reference number: I57716; MUID:95021301; PMID:7935485

A;Accession: I57716

A;Status: translation not shown; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-22 <CAV2>

A;Cross-references: GB:S74689; NID:g786350; PIDN:AAD14156.1; PID:g4261856

R;Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Erickson, J.W.
submitted to the Brookhaven Protein Data Bank, April 1993
A;Reference number: A51839; PDB:1LYA
A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 65-161;170-241
R;Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Erickson, J.W.
submitted to the Brookhaven Protein Data Bank, April 1993
A;Reference number: A51840; PDB:1LYB
A;Contents: annotation; X-ray crystallography, 2.5 angstroms, with inhibitor residues 65-161;170-241
R;Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Hosur, M.V.; Sowder II, R.C.; Cachau, R.E.; Collins, J.; Silva, A.M.; Erickson, J.W.
Proc. Natl. Acad. Sci. U.S.A. 90, 6796-6800, 1993
A;Title: Crystal structures of native and inhibited forms of human cathepsin D: implications for lysosomal targeting and drug design.
A;Reference number: A48229; MUID:93342076; PMID:8393577
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Comment: Cathepsin D is a ubiquitous lysosomal proteinase.
C;Comment: In addition to the propeptide, residues 163-168 and 411-412 are proteolytically removed. Residues 169 and 170 are also partially removed.
C;Comment: The carbohydrate bound to 134-Asn contains a mannose-6-phosphate that is bound near 267-Lys and the phosphotransferase recognition region.
C;Genetics:
A;Gene: GDB:CTSD
A;Cross-references: GDB:120512; OMIM:116840
A;Map position: 11p15.5-11p15.5
C;Function:
A;Description: limited specificity endopeptidase
A;Pathway: intracellular protein degradation
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-64/Domain: propeptide #status predicted <PRO>
F;65-162,169-410/Product: cathepsin D #status experimental <MAT>
F;267,329-356/Region: phosphotransferase recognition
F;91-160,110-117,286-290,329-366/Disulfide bonds: #status experimental
F;97,295/Active site: Asp #status experimental
F;134,263/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 11.5%; Score 308.5; DB 1; Length 412;
Best Local Similarity 27.1%; Pred. No. 2.5e-15;
Matches 121; Conservative 75; Mismatches 180; Indels 71; Gaps 22;

```

Qy      9 LLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPG-----PGTPAERHADGLAL 62
      | | | |   | | | | | | : | |   : | : : |   |   : : : :
Db      6 LLPLAL--CLLAAP--ASALVRIPLHKFTSIRRTMSEVGGSVEDLIAKGPVSKYSQAVPA 61

Qy     63 ALEPALASPAGAAFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP 122
      | : |   | : :   | | | : | | | | |   : : | | | | | |
Db     62 VTEGPI--PEVLKNYM-----DAQYYGEIGIGTPPQCFTVVFDTGSSNLWVPSIH 109

Qy    123 HSYIDT-----YFDTERSSTYRSKGFVDTVKYTGQSWTGFVGEDLVTIP--KGFNTSFL 174
      : |   : : : : | | | |   | : | | | : : : : | | : : | |
Db    110 CKLLDIACWIHHKYNSDKSSTYVKNGTSFDIHYGSGSLSGYLSQDTSVSPCQSASSASAL 169

Qy    175 --VNIATIFESENFFLPGI-----KWNIGILGLAYATLAKPSSSLETFFDSLVTQANI-PN 226

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      | :      |      |||      |::|||::||      ::      ::      ||::| : | : |
Db      170 GGVKVERQVFGEATKQPGITFIAAKFDGILGMAYPRIS--VNNVLPVFDNLMQQKLVDQN 227

Qy      227 VFQMCMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQ 286
      :||      |      || |::|| :      ||| : | : : |:: : ::|:
Db      228 IFSFY-----LSRDPDAQPGGELMLGGTDSKYYKGSLSYLNVTRKAYWQVHLDQVEV-AS 281

Qy      287 SLNLDCREYNADKAIVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQIACWT 346
      | | |::| :|||::||:| :      | | |      :| :      : |
Db      282 GLTL-CKE--GCEAIVDTGTSLMVGP---VDEVRELQKAIGAVPLIQGEY----MIPC--- 329

Qy      347 NSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRF---GISPSTN 403
      | | |::| :      : ::| : | : |      |      | | :
Db      330 ---EKVSTLPAITLKL----GGKGKLS--PEDYTLKVSQAGKTLCLSGFMGMDIPPPSG 380

Qy      404 AL-VIGATVMEGFYVIFDRAQKRVGFA 429
      | ::| : : | :|||      ||||
Db      381 PLWILGDVFIGRYYTVFDRDNNRVGFA 407

```

RESULT 15

KHMSD

cathepsin D (EC 3.4.23.5) precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999

C;Accession: I48278; S14704; S12587

R;Hetman, M.; Perschl, A.; Saftig, P.; Von Figura, K.; Peters, C.

DNA Cell Biol. 13, 419-427, 1994

A;Title: Mouse cathepsin D gene: molecular organization, characterization of the promoter, and chromosomal localization.

A;Reference number: I48278; MUID:94280622; PMID:8011168

A;Accession: I48278

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-410 <RES>

A;Cross-references: EMBL:X68378; NID:g50302; PIDN:CAA48453.1; PID:g817945

R;Diedrich, J.F.; Staskus, K.A.; Retzel, E.F.; Haase, A.T.

Nucleic Acids Res. 18, 7184, 1990

A;Title: Nucleotide sequence of a cDNA encoding mouse cathepsin D.

A;Reference number: S14704; MUID:91088345; PMID:2263503

A;Accession: S14704

A;Molecule type: mRNA

A;Residues: 1-410 <DIE>

A;Cross-references: EMBL:X53337; NID:g50300; PIDN:CAA37423.1; PID:g50301

R;Grusby, M.J.; Mitchell, S.C.; Glimcher, L.H.

Nucleic Acids Res. 18, 4008, 1990

A;Title: Molecular cloning of mouse cathepsin D.

A;Reference number: S12587; MUID:90326544; PMID:2374732

A;Accession: S12587

A;Molecule type: mRNA

A;Residues: 1-410 <GRU>

A;Cross-references: EMBL:X52886; NID:g50298; PIDN:CAA37067.1; PID:g50299

C;Genetics:

A;Introns: 23/2; 76/3; 118/1; 157/3; 233/2; 274/2; 322/3; 355/3

C;Function:

A;Description: limited specificity endopeptidase

A;Pathway: intracellular protein degradation

C;Superfamily: pepsin
 C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-64/Domain: propeptide #status predicted <PRO>
 F;65-410/Product: cathepsin D, single-chain form #status predicted <MAT>
 F;91-160,110-117,284-288,327-364/Disulfide bonds: #status predicted
 F;97,293/Active site: Asp #status predicted
 F;134,261/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.4%; Score 306.5; DB 1; Length 410;
 Best Local Similarity 27.5%; Pred. No. 3.6e-15;
 Matches 103; Conservative 64; Mismatches 123; Indels 85; Gaps 15;

```

Qy      92 YYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDT-----YFDTERSSTYRSKGFVDV 145
      || :: ||||| :: ||||| | :| ::::||| |
Db      79 YYGDIGIGTPPQCFTVVFDTGSSNLWVPSIHCKILDIACWVHHKYNDSKSSTYVKNGTSTF 138

Qy     146 TVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIAT---IFESENFFLPGI-----KWNIGIL 197
      : | || :::: :| |::| : | | | | | | | | | | | | | | | | | | | | | |
Db     139 DIHYGSGSLSGYLSQDITVSVPCSDQSKARGIKVEKQIF-GEATKQPGIVFVAAKFDGIL 197

Qy     198 GLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEP 256
      |: | :: :::: ||::| : | : | | | | | | | | | | | | | | | | | | | | | |
Db     198 GMGYPHIS--VNNVLPVFDNLMQQKLVDKNIFSFY-----LNRDPEGQPGGELMLGGTDS 250

Qy     257 SLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVF 316
      | |:: | : : |::: : ||:| : | | | : : ||::||:| | : |
Db     251 KYYHGELSYLNVTRKAYWQVHMDQLEVGNE-LTL-CK--GGCEAIVDTGTSLLVGPVEEV 306

Qy     317 DAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSRRSFRITIL 376
      : :|: || : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     307 KELQKAIGAVPLI-----QGEYMIPCEKVSSL 333

Qy     377 POLYIQPMMGAGLNYEC----YRFGIS-----PSTNALVIGATVMEG 414
      | :|:: :| | || | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     334 PTVYLK--LG-GKNYELHPDKYILKVSQGGKTICLSGFMGMDIPPPSGPLWILGDVFIGS 390

Qy     415 FYVIFDRAQKRVGFA 429
      :| :||| ||||
Db     391 YYTVFDRDNNRVGFA 405
  
```

Search completed: February 28, 2004, 09:11:59
 Job time : 19.5 secs

OM protein - protein search, using sw model

Run on: February 28, 2004, 08:57:15 ; Search time 11.7727 Seconds
(without alignments)
2291.087 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALARALLLPLLAQWLLRA.....RPRDPEVVNDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2687	100.0	518	1	BAE2_HUMAN	Q9y5z0	homo sapien
2	1187	44.2	501	1	BACE_RAT	P56819	rattus norv
3	1185	44.1	501	1	BACE_MOUSE	P56818	mus musculu
4	1178.5	43.9	501	1	BACE_HUMAN	P56817	homo sapien
5	363.5	13.5	377	1	PEPC_MACFU	P03955	macaca fusc
6	353	13.1	388	1	PEPC_HUMAN	P20142	homo sapien
7	351.5	13.1	388	1	PEPC_CALJA	Q9n2d3	callithrix
8	324.5	12.1	394	1	PEPC_CAVPO	Q64411	cavia porce
9	320	11.9	402	1	RENI_MOUSE	P06281	mus musculu
10	315.5	11.7	396	1	CATD_CLUHA	Q9dex3	clupea hare
11	313.5	11.7	509	1	APR1_ORYSA	Q42456	oryza sativ
12	313	11.6	392	1	PEPC_RAT	P04073	rattus norv
13	310	11.5	383	1	PEPE_CHICK	P16476	gallus gall
14	308.5	11.5	412	1	CATD_HUMAN	P07339	homo sapien
15	306.5	11.4	410	1	CATD_MOUSE	P18242	mus musculu
16	305.5	11.4	401	1	RENS_MOUSE	P00796	mus musculu
17	305	11.4	407	1	CATD_RAT	P24268	rattus norv

18	302	11.2	324	1	PEP1_GADMO	P56272	gadus morhu
19	302	11.2	405	1	CARP_YEAST	P07267	saccharomyc
20	301.5	11.2	398	1	CATE_RAT	P16228	rattus norv
21	300.5	11.2	387	1	PEP2_RABIT	P27821	oryctolagus
22	300.5	11.2	397	1	CATE_MOUSE	P70269	mus musculu
23	299	11.1	398	1	CATD_CHICK	Q05744	gallus gall
24	298.5	11.1	387	1	PEP4_RABIT	P28713	oryctolagus
25	298.5	11.1	400	1	RENI_SHEEP	P52115	ovis aries
26	297	11.1	388	1	PEPA_HUMAN	P00790	homo sapien
27	294.5	11.0	388	1	PEP2_MACFU	P27677	macaca fusc
28	291	10.8	388	1	PEP4_MACFU	P27678	macaca fusc
29	291	10.8	402	1	RENI_RAT	P08424	rattus norv
30	291	10.8	406	1	RENI_HUMAN	P00797	homo sapien
31	291	10.8	406	1	RENI_PANTR	P60016	pan troglod
32	290.5	10.8	396	1	CATE_RABIT	P43159	oryctolagus
33	289	10.8	387	1	PEP3_RABIT	P27822	oryctolagus
34	289	10.8	388	1	PAG_HORSE	Q28389	equus cabal
35	288.5	10.7	390	1	CATD_BOVIN	P80209	bos taurus
36	288	10.7	387	1	PEP1_RABIT	P28712	oryctolagus
37	288	10.7	388	1	PEP1_MACFU	P03954	macaca fusc
38	287	10.7	367	1	PEPA_CHICK	P00793	gallus gall
39	287	10.7	391	1	CATE_CAVPO	P25796	cavia porce
40	287	10.7	396	1	CATE_HUMAN	P14091	homo sapien
41	286	10.6	388	1	PEPA_MACMU	P11489	macaca mula
42	285.5	10.6	387	1	PEPA_CALJA	Q9n2d4	callithrix
43	285	10.6	396	1	CARP_NEUCR	Q01294	neurospora
44	284.5	10.6	386	1	PEPA_PIG	P00791	sus scrofa
45	283	10.5	388	1	PEPF_RABIT	P27823	oryctolagus

ALIGNMENTS

RESULT 1

BAE2_HUMAN

ID BAE2_HUMAN STANDARD; PRT; 518 AA.
AC Q9Y5Z0; Q9UJT6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta secretase 2 precursor (EC 3.4.23.45) (Beta-site APP-cleaving
DE enzyme 2) (Aspartyl protease 1) (Asp 1) (ASP1) (Membrane-associated
DE aspartic protease 1) (Memapsin-1) (Down region aspartic protease).
GN BACE2 OR ASP21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057170; PubMed=10591213;
RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
RT "Membrane-anchored aspartyl protease with Alzheimer's disease
RT beta-secretase activity.";
RL Nature 402:533-537(1999).

RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Xin H., Stephans J.C., Duan X., Harrowe G., Kim E., Grieshammer U.,
 RA Giese K.;
 RT "Identification of a novel aspartic-like protease differentially
 RT expressed in human breast cancer cell lines.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.;
 RT "Cloning of a gene from chromosome 21 Down region encoding a potential
 RT transmembrane aspartyl protease.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Solans A., Estivill X., de la Luna S.;
 RT "Cloning of a novel mammalian aspartyl protease.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20120043; PubMed=10656250;
 RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
 RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic proteinase (Asp 2) as
 RT beta-secretase.";
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20144060; PubMed=10677483;
 RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20289799; PubMed=10830953;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
 RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
 RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
 RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Lehrach H., Reinhardt R., Yaspo M.-L.;
 RT "The DNA sequence of human chromosome 21.";
 RL Nature 405:311-319(2000).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [9]

RP CHARACTERIZATION.

RX MEDLINE=22088158; PubMed=12093293;

RA Turner R.T. III, Loy J.A., Nguyen C., Devasamudram T., Ghosh A.K.,
 RA Koelsch G., Tang J.;

RT "Specificity of memapsin 1 and its implications on the design of
 RT memapsin 2 (beta-secretase) inhibitor selectivity.";

RL Biochemistry 41:8742-8746(2002).

CC -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to peptidase family A1.

CC -----
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DR EMBL; AF200342; AAF17078.1; -.

DR EMBL; AF117892; AAD45240.1; -.

DR EMBL; AF050171; AAD45963.1; -.

DR EMBL; AF178532; AAF29494.1; -.

DR EMBL; AF204944; AAF26368.1; -.

DR EMBL; AF200192; AAF13714.1; -.

DR EMBL; AL163284; CAB90458.1; -.

DR EMBL; AL163285; CAB90554.1; -.

DR EMBL; BC014453; AAH14453.1; -.

DR HSSP; P00797; 2REN.

DR MEROPS; A01.041; -.

DR Genew; HGNC:934; BACE2.

DR MIM; 605668; -.

DR GO; GO:0005624; C:membrane fraction; TAS.

DR GO; GO:0004190; F:aspartic-type endopeptidase activity; TAS.

DR GO; GO:0006464; P:protein modification; TAS.

DR GO; GO:0009306; P:protein secretion; TAS.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 ? POTENTIAL.
 FT CHAIN ? 518 BETA SECRETASE 2.
 FT DOMAIN 21 473 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 474 494 POTENTIAL.
 FT DOMAIN 495 518 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 110 110 BY SIMILARITY.
 FT ACT_SITE 303 303 BY SIMILARITY.
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 36 36 A -> T (IN REF. 6).
 SQ SEQUENCE 518 AA; 56180 MW; 2E903150823760D3 CRC64;

Query Match 100.0%; Score 2687; DB 1; Length 518;
 Best Local Similarity 100.0%; Pred. No. 2e-187;
 Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP	60
Qy	61	ALALEPALASPAGAAANFLAMVDNLQGDSSRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAAANFLAMVDNLQGDSSRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Qy	241	GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA	300
Db	241	GSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA	300
Qy	301	IVDSGTTLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI	360
Qy	361	YLRDENSSRSFRITILPQLYIQPMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Db	361	YLRDENSSRSFRITILPQLYIQPMAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420
Qy	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480
Db	421	RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG	480

Qy 481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518
 |||
 Db 481 AILLVLIVLLLLPFRQCRRPRDPEVVNDESSLVRHRWK 518

RESULT 2

BACE_RAT

ID BACE_RAT STANDARD; PRT; 501 AA.
 AC P56819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Beta-secretase precursor (EC 3.4.23.46) (Beta-site APP cleaving
 DE enzyme) (Beta-site amyloid precursor protein cleaving enzyme)
 DE (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
 DE protease 2) (Memapsin-2).
 GN BACE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20002972; PubMed=10531052;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.;
 RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).
 CC -!- FUNCTION: Responsible for the proteolytic processing of the
 CC amyloid precursor protein (APP). Cleaves at the amino terminus of
 CC the A-beta peptide sequence, between residues 671 and 672 of APP,
 CC leads to the generation and extracellular release of beta-cleaved
 CC soluble APP, and a corresponding cell-associated carboxy-terminal
 CC fragment which is later release by gamma-secretase (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; AF190727; AAF04144.1; -.
 DR HSSP; P32329; 1YPS.
 DR MEROPS; A01.004; -.
 DR InterPro; IPR001969; Aspprotease_AS.

DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 45 POTENTIAL.
 FT CHAIN 46 501 BETA-SECRETASE.
 FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 458 478 POTENTIAL.
 FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 93 93 BY SIMILARITY.
 FT ACT_SITE 289 289 BY SIMILARITY.
 FT DISULFID 216 420 BY SIMILARITY.
 FT DISULFID 278 443 BY SIMILARITY.
 FT DISULFID 330 380 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55806 MW; 24B445BC8BE87DE3 CRC64;

Query Match 44.2%; Score 1187; DB 1; Length 501;
 Best Local Similarity 46.4%; Pred. No. 1.2e-78;
 Matches 240; Conservative 82; Mismatches 165; Indels 30; Gaps 9;

Qy 9 LLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTPGP--GTPAERHADGLA 61
 : | | | : | | | | | | | | | | | | | | | | | |
 Db 1 MAPALRWLLWVGSGMLPAQGTHLGIRLPLRSGLA-----GPPLGLRLPRETDE-- 49
 Qy 62 LALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGT 121
 | | | : | | | | | | | | | | | | | | | | | |
 Db 50 ---EP--EEPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPQTLNILVDTGSSNFAVGAA 104
 Qy 122 PHSYIDTYFDTERSSTYRSKGFVDVTVKYTQGSWTGFVGEDLVTPKGFNTSFLVNIATIF 181
 | | : : | : | | | | | | | | | | | | | | | | | |
 Db 105 PHPFLHRYYQRLSSTYRDLRKSVMYPYTQGWEGELGTDLVSIHPGNVTVRANIAAIT 164
 Qy 182 ESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFMSMQMCGAGLPV-- 239
 | : | : | | | | | | | : | | | | | | | : | : | : | : | : | : | : |
 Db 165 ESDKFFINGSNWEIGILGLAYAEIARPDDSLPFFDSLVKQTHIPNIFSLQLCGAGFPLNQ 224
 Qy 240 -AGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNAD 298
 : | | : : | : | | | : | | | : | | : | : | : | : | : | : | : |
 Db 225 TEALASVGGSMIIGGIDHSLYTGSLWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYD 284
 Qy 299 KAIVDSGTTLRLRPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPMKI 358
 | : | | | | | | | : | : | : | : | : | : | : | : | : | : | : |
 Db 285 KSIVDSGTTLRLRPKKVFEEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVI 344
 Qy 359 SIYLRDENSSRSFRITILPOLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYV 417
 | : | | | : : | | | | | | | : : | : : | : | : | : | : | : | : |
 Db 345 SLYLMGEVTNQSFRTILPQQYLRPVEDVATSDDCYKFAVSQSSTGTVMGAVIMEGFYV 404
 Qy 418 IFDRAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMS 477

```

          :||||:|:| | | | : : ||| | | : | | :| : :
Db      405 VFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAA 464

Qy      478 VCGAILLVLLIVLLLLPFRQQR--RPRDPEVVNDESSL 512
          :| |: : : |: : :|| | | : : :| | |
Db      465 IC-ALFMLPLCLMVCQWRCLRLRHQHDDFADDISLL 500

```

RESULT 3

BACE_MOUSE

```

ID      BACE_MOUSE      STANDARD;      PRT;      501 AA.
AC      P56818;
DT      30-MAY-2000 (Rel. 39, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Beta-secretase precursor (EC 3.4.23.46) (Beta-site APP cleaving
DE      enzyme) (Beta-site amyloid precursor protein cleaving enzyme)
DE      (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
DE      protease 2) (Memapsin-2).
GN      BACE.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20002972; PubMed=10531052;
RA      Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
RA      Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,
RA      Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
RA      Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
RA      Treanor J., Rogers G., Citron M.;
RT      "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
RT      the transmembrane aspartic protease BACE.";
RL      Science 286:735-741(1999).
RN      [2]
RP      REVISIONS TO 6 AND 81-87.
RA      Bennett B.D., Vassar R., Citron M.;
RL      Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20057170; PubMed=10591213;
RA      Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
RA      Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
RA      Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
RT      "Membrane-anchored aspartyl protease with Alzheimer's disease
RT      beta-secretase activity.";
RL      Nature 402:533-537(1999).
CC      -!- FUNCTION: Responsible for the proteolytic processing of the
CC      amyloid precursor protein (APP). Cleaves at the amino terminus of
CC      the A-beta peptide sequence, between residues 671 and 672 of APP,
CC      leads to the generation and extracellular release of beta-cleaved
CC      soluble APP, and a corresponding cell-associated carboxy-terminal
CC      fragment which is later release by gamma-secretase (By
CC      similarity).
CC      -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
CC      Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of

```

CC Alzheimer's amyloid precursor protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; AF190726; AAF04143.2; -.
 DR EMBL; AF200346; AAF17082.1; -.
 DR HSSP; P56272; 1AM5.
 DR MEROPS; A01.004; -.
 DR MGD; MGI:1346542; Bace.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Transmembrane;
 KW Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT PROPEP 22 45 POTENTIAL.
 FT CHAIN 46 501 BETA-SECRETASE.
 FT DOMAIN 22 457 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 458 478 POTENTIAL.
 FT DOMAIN 479 501 CYTOPLASMIC (POTENTIAL).
 FT ACT_SITE 93 93 BY SIMILARITY.
 FT ACT_SITE 289 289 BY SIMILARITY.
 FT DISULFID 216 420 BY SIMILARITY.
 FT DISULFID 278 443 BY SIMILARITY.
 FT DISULFID 330 380 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 501 AA; 55747 MW; C085A013145E474E CRC64;

Query Match 44.1%; Score 1185; DB 1; Length 501;
 Best Local Similarity 46.0%; Pred. No. 1.7e-78;
 Matches 237; Conservative 83; Mismatches 169; Indels 26; Gaps 7;

Qy 9 LLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTPGPGTPAERHADGLALA 63
 : | | | : | | | | | | | | :
 Db 1 MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLA-----GPPLGLRLPRETDEES----- 51
 Qy 64 LEPALASPAGAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPH 123
 | : | : | | | : | | : | | | : | | | | | | | |
 Db 52 -----EEPGRGGSFVEMVDNLRGKSGQGYVEMTVGSPQTNLNVLDTGSSNFAVGAAPH 106
 Qy 124 SYIDTYFDTERSSTYRSKGFVDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFES 183
 :: | : : | | | | | | | | | | : | | : | | | | |

Db 107 PFLHRYYQRQLSSTYRDLRKGVYVPYTQGWEGELGTDLVSIPHGPNVTVRANIAAITES 166

Qy 184 ENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV---A 240
: ||: | | ||||| :|:| ||| ||||| | :||:|:|:|:| ||: |:

Db 167 DKFFINGSNWEGILGLAYAEIARDDSLPFFDSLQTHIPNIFSLQLCGAGFPLNQTE 226

Qy 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDREYNADKA 300
: |||:|:|:|:| ||| | :|||:|:|:|:|:| |:|:|:| ||: |:

Db 227 ALASVGGSMIIGGIDHSLYTGSWYTPIRREWYEVIIVRVEINGQDLKMDCKEYNYDKS 286

Qy 301 IVDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
||| ||| |||:|:|:| |:|:| || | ||| | || || |||: || ||:

Db 287 IVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISL 346

Qy 361 YLRDENSSRSFRITILPQLYIQPMGAGLNY-ECYRFGISPSTNALVIGATVMGEGFYVIF 419
|| | :|:|:|:|:| ||:|:| : |:|:| | | : |:| :|:|:|:|:

Db 347 YLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFIYVVF 406

Qy 420 DRAQKRVGFAAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVC 479
|||:|:|:| | | : : ||| | | : | | :|:| : :|

Db 407 DRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAAIC 466

Qy 480 GAILLVLLVLLLLPFRQCR--RPRDPEVVNDESSL 512
|: : : |: : :|| | | : : :| | |

Db 467 -ALFMLPLCLMVCQWRCLRLRHQHDDFADDISLL 500

RESULT 4

BACE_HUMAN

ID BACE_HUMAN STANDARD; PRT; 501 AA.

AC P56817; Q9BYB9; Q9BYC0; Q9BYC1; Q9UJT5;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Beta-secretase precursor (EC 3.4.23.46) (Beta-site APP cleaving enzyme) (Beta-site amyloid precursor protein cleaving enzyme)

DE (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2) (Memapsin-2).

GN BACE OR BACE1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM A).

RC TISSUE=Brain;

RX MEDLINE=20002972; PubMed=10531052;

RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,

RA Denis P., Teplow D.B., Ross S., Amarante P., Loeloff R., Luo Y.,

RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,

RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,

RA Treanor J., Rogers G., Citron M.;

RT "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by the transmembrane aspartic protease BACE.";

RL Science 286:735-741(1999).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND

RP CHARACTERIZATION.
 RC TISSUE=Brain;
 RX MEDLINE=20057171; PubMed=10591214;
 RA Sinha S., Anderson J.P., Barbour R., Basi G.S., Caccavello R.,
 RA Davis D., Doan M., Dovey H.F., Frigon N., Hong J., Jacobson-Croak K.,
 RA Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,
 RA Tatsuno G., Tung J., Schenk D., Seubert P., Suomensaaari S.M., Wang S.,
 RA Walker D., Zhao J., McConlogue L., Varghese J.;
 RT "Purification and cloning of amyloid precursor protein beta-secretase
 RT from human brain.";
 RL Nature 402:537-540(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20057170; PubMed=10591213;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
 RA Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
 RT secretase activity.";
 RL Nature 402:533-537(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20120043; PubMed=10656250;
 RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
 RA Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
 RT secretase.";
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RC TISSUE=Brain, and Pancreas;
 RA Michel B., De Pietri Tonelli D., Zacchetti D., Keller P.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1B) obtained from
 RT human brain and pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM C).
 RC TISSUE=Pancreas;
 RA Zacchetti D., De Pietri Tonelli D., Schnurbus R.;
 RT "New beta-site APP cleaving enzyme isoform (BACE-1C) obtained from
 RT human pancreas.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
 RC TISSUE=Brain;
 RX MEDLINE=21408467; PubMed=11516562;
 RA Tanahashi H., Tabira T.;
 RT "Three novel alternatively spliced isoforms of the human beta-site
 RT amyloid precursor protein cleaving enzyme (BACE) and their effect on
 RT amyloid beta-peptide production.";
 RL Neurosci. Lett. 307:9-12(2001).
 RN [8]
 RP SEQUENCE OF 14-501 FROM N.A. (ISOFORM A), AND CHARACTERIZATION.
 RX MEDLINE=20144060; PubMed=10677483;
 RA Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of

RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=21950860; PubMed=11953458;
 RA Fischer F., Molinari M., Bodendorf U., Paganetti P.;
 RT "The disulphide bonds in the catalytic domain of BACE are critical but
 RT not essential for amyloid precursor protein processing activity.";
 RL J. Neurochem. 80:1079-1088(2002).
 CC -!- FUNCTION: Responsible for the proteolytic processing of the
 CC amyloid precursor protein (APP). Cleaves at the amino terminus of
 CC the A-beta peptide sequence, between residues 671 and 672 of APP,
 CC leads to the generation and extracellular release of beta-cleaved
 CC soluble APP, and a corresponding cell-associated carboxy-terminal
 CC fragment which is later release by gamma-secretase.
 CC -!- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Asn-Leu-|-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=A; Synonyms=BACE-1A, BAC-501;
 CC IsoId=P56817-1; Sequence=Displayed;
 CC Name=B; Synonyms=BACE-1B, BACE-I-476;
 CC IsoId=P56817-2; Sequence=VSP_005223;
 CC Name=C; Synonyms=BACE-1C, BACE-I-457;
 CC IsoId=P56817-3; Sequence=VSP_005222;
 CC Name=D; Synonyms=BACE-1D, BACE-I-432;
 CC IsoId=P56817-4; Sequence=VSP_005222, VSP_005223;
 CC -!- TISSUE SPECIFICITY: Brain.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; AF190725; AAF04142.1; -.
 DR EMBL; AF201468; AAF18982.1; -.
 DR EMBL; AF200343; AAF17079.1; -.
 DR EMBL; AF204943; AAF26367.1; -.
 DR EMBL; AF338816; AAK38374.1; -.
 DR EMBL; AF338817; AAK38375.1; -.
 DR EMBL; AB050436; BAB40931.1; -.
 DR EMBL; AB050437; BAB40932.1; -.
 DR EMBL; AB050438; BAB40933.1; -.
 DR EMBL; AF200193; AAF13715.1; -.
 DR PIR; A59090; A59090.
 DR PDB; 1M4H; 28-AUG-02.
 DR MEROPS; A01.004; -.
 DR Genew; HGNC:933; BACE.
 DR MIM; 604252; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0008798; F:beta-aspartyl-peptidase activity; TAS.

Db 283 YDKSIVDSGTTNLRPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFP 342
 Qy 357 KISIYLRDENSSRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGF 415
 ||:|| | :::||||||| |::| : :||:| || |: |:| :|||
 Db 343 VISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 402
 Qy 416 YVIFDRAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYAL 475
 ||:||||:|:| | | : : || | | : | | :| :
 Db 403 YVVFDRAKRGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDESTLMTIAYVM 462
 Qy 476 MSVCGAILLVLLVLLLLPFRQR--RPRDPEVVNDESSL 512
 ::| |: : : |: : || | | : : :| | |
 Db 463 AAIC-ALFMLPLCLMVCQWRCLRLRQQHDDFADDISLL 500

RESULT 5

PEPC_MACFU

ID PEPC_MACFU STANDARD; PRT; 377 AA.
 AC P03955;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C) (Fragment).
 GN PGC.
 OS Macaca fuscata fuscata (Japanese macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9543;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Gastric mucosa;
 RX MEDLINE=92037645; PubMed=1935977;
 RA Kageyama T., Tanabe K., Koiwai O.;
 RT "Development-dependent expression of isozymogens of monkey
 RT pepsinogens and structural differences between them.";
 RL Eur. J. Biochem. 202:205-215(1991).
 RN [2]
 RP SEQUENCE OF 6-377.
 RX MEDLINE=86168133; PubMed=3514597;
 RA Kageyama T., Takahashi K.;
 RT "The complete amino acid sequence of monkey progastricsin.";
 RL J. Biol. Chem. 261:4406-4419(1986).
 RN [3]
 RP SEQUENCE OF 6-65.
 RX MEDLINE=85289106; PubMed=3928607;
 RA Kageyama T., Takahashi K.;
 RT "Monkey pepsinogens and pepsins. VII. Analysis of the activation
 RT process and determination of the NH2-terminal 60-residue sequence of
 RT Japanese monkey progastricsin, and molecular evolution of
 RT pepsinogens.";
 RL J. Biochem. 97:1235-1246(1985).
 CC -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr-Xaa bonds; high activity
 CC towards hemoglobin as substrate.
 CC -!- PTM: Each pepsinogen is converted to corresponding pepsin at pH
 CC 2.0 in part as a result of the release of a 47 aa activation


```

Db      193 ALTSPIFSVYLSLSDQ-----QGSSGGAVVFGGVDSSSLYTGQIYWAPVTQELYWQIGIEEF 246
Qy      282 EIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ 341
      ||||:  | |  :||||:|:| | :||:  |::|  ||:|
Db      247 LIGGQASGW-CSE--GCQAIVDTGTSLTVPQQYMSALLQA-----TGAQ 288
Qy      342 LACWTNSETPWSYF-----PKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNY 391
      | : |  | : :  : | ||  ||
Db      289 -----EDEYGGQFLVNCNSIQNLPTLTFTII-----NGVEFPLPPSSYI-----LNN 328
Qy      392 ECY-RFGISP-----STNALVIGATVMEGFYVIFDRAQKRVGF AAS 431
      | | : |  | : : | : : | : |||| :
Db      329 NGYCTVGVEPTYLSAQNSQPLWILGDVFLRSYYSVYDLSNNRVGFATA 376

```

RESULT 6

PEPC_HUMAN

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ID      PEPC_HUMAN      STANDARD;      PRT;      388 AA.
AC      P20142;
DT      01-FEB-1991 (Rel. 17, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
GN      PGC.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88087276; PubMed=3335549;
RA      Hayano T., Sogawa K., Ichihara Y., Fujii-Kuriyama Y., Takahashi K.;
RT      "Primary structure of human pepsinogen C gene.";
RL      J. Biol. Chem. 263:1382-1385(1988).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89079679; PubMed=2909526;
RA      Taggart R.T., Cass L.G., Mohandas T.K., Derby P., Barr P.J., Pals G.,
RA      Bell G.I.;
RT      "Human pepsinogen C (progastricsin). Isolation of cDNA clones,
RT      localization to chromosome 6, and sequence homology with pepsinogen
RT      A.";
RL      J. Biol. Chem. 264:375-379(1989).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Placenta;
RX      MEDLINE=89290840; PubMed=2567697;
RA      Pals G., Azuma T., Mohandas T.K., Bell G.I., Bacon J.,
RA      Samloff I.M., Walz D.A., Barr P.J., Taggart R.T.;
RT      "Human pepsinogen C (progastricsin) polymorphism: evidence for a
RT      single locus located at 6p21.1-pter.";
RL      Genomics 4:137-148(1989).
RN      [4]
RP      SEQUENCE FROM N.A.
RA      Wong R.N.S., Tang J.;
RL      Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN      [5]

```

RP SEQUENCE OF 17-101.
RX MEDLINE=90130402; PubMed=2515193;
RA Athauda S.B.P., Tanji M., Kageyama T., Takahashi K.;
RT "A comparative study on the NH2-terminal amino acid sequences and
RT some other properties of six isozymic forms of human pepsinogens and
RT pepsins.";
RL J. Biochem. 106:920-927(1989).
RN [6]
RP SEQUENCE OF 17-64.
RX MEDLINE=83079318; PubMed=6816595;
RA Foltmann B., Jensen A.L.;
RT "Human progastricsin. Analysis of intermediates during activation
RT into gastricsin and determination of the amino acid sequence of the
RT propart.";
RL Eur. J. Biochem. 128:63-70(1982).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.62 ANGSTROMS).
RX MEDLINE=95230687; PubMed=7714902;
RA Moore S.A., Sielecki A.R., Chernai M.M., Tarasova N.I., James M.N.G.;
RT "Crystal and molecular structures of human progastricsin at 1.62-A
RT resolution.";
RL J. Mol. Biol. 247:466-485(1995).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.36 ANGSTROMS).
RX MEDLINE=98069649; PubMed=9406551;
RA Khan A.R., Cherney M.M., Tarasova N.I., James M.N.;
RT "Structural characterization of activation 'intermediate 2' on the
RT pathway to human gastricsin.";
RL Nat. Struct. Biol. 4:1010-1015(1997).
CC -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
CC shows preferential cleavage at Tyr-Xaa bonds; high activity
CC towards hemoglobin as substrate.
CC -!- SIMILARITY: Belongs to peptidase family A1.

CC -----
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CC -----

DR EMBL; M18667; AAA60062.1; ALT_INIT.
DR EMBL; M18659; AAA60062.1; JOINED.
DR EMBL; M18660; AAA60062.1; JOINED.
DR EMBL; M18661; AAA60062.1; JOINED.
DR EMBL; M18662; AAA60062.1; JOINED.
DR EMBL; M18663; AAA60062.1; JOINED.
DR EMBL; M18664; AAA60062.1; JOINED.
DR EMBL; M18665; AAA60062.1; JOINED.
DR EMBL; M18666; AAA60062.1; JOINED.
DR EMBL; M23077; AAA60063.1; -.
DR EMBL; M23069; AAA60063.1; JOINED.
DR EMBL; M23070; AAA60063.1; JOINED.
DR EMBL; M23071; AAA60063.1; JOINED.
DR EMBL; M23072; AAA60063.1; JOINED.
DR EMBL; M23073; AAA60063.1; JOINED.

DR EMBL; M23074; AAA60063.1; JOINED.
 DR EMBL; M23075; AAA60063.1; JOINED.
 DR EMBL; J04443; AAA60074.1; -.
 DR EMBL; U75272; AAB18273.1; -.
 DR PIR; A29937; A29937.
 DR PDB; 1HTR; 26-JAN-95.
 DR PDB; 1AVF; 25-FEB-98.
 DR MEROPS; A01.003; -.
 DR Genew; HGNC:8890; PGC.
 DR MIM; 169740; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; TAS.
 DR GO; GO:0007586; P:digestion; TAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal;
 KW 3D-structure.
 FT SIGNAL 1 16
 FT PROPEP 17 59 ACTIVATION PEPTIDE.
 FT CHAIN 60 388 GASTRICSIN.
 FT ACT_SITE 91 91
 FT ACT_SITE 276 276
 FT DISULFID 104 109
 FT DISULFID 267 271
 FT DISULFID 310 343
 FT CONFLICT 40 41 GE -> ED (IN REF. 6).
 FT CONFLICT 52 52 W -> S (IN REF. 6).
 FT STRAND 19 25
 FT HELIX 29 35
 FT TURN 36 37
 FT HELIX 39 43
 FT TURN 44 45
 FT HELIX 50 54
 FT HELIX 65 68
 FT TURN 69 70
 FT STRAND 73 79
 FT TURN 80 83
 FT STRAND 84 91
 FT TURN 92 93
 FT STRAND 97 101
 FT TURN 102 103
 FT HELIX 107 110
 FT TURN 111 111
 FT STRAND 115 115
 FT HELIX 117 119
 FT TURN 121 122
 FT STRAND 124 134
 FT TURN 135 136
 FT STRAND 137 150
 FT TURN 151 152
 FT STRAND 153 163
 FT HELIX 169 173

FT	STRAND	178	181
FT	TURN	190	191
FT	HELIX	195	201
FT	TURN	202	203
FT	STRAND	209	214
FT	STRAND	221	227
FT	HELIX	232	234
FT	STRAND	235	244
FT	STRAND	251	254
FT	STRAND	256	259
FT	TURN	260	261
FT	STRAND	262	263
FT	TURN	266	269
FT	STRAND	271	275
FT	TURN	277	278
FT	STRAND	282	285
FT	HELIX	286	288
FT	HELIX	289	296
FT	TURN	297	297
FT	STRAND	299	300
FT	TURN	302	303
FT	STRAND	306	308
FT	HELIX	310	315
FT	STRAND	319	323
FT	TURN	324	325
FT	STRAND	326	330
FT	HELIX	332	335
FT	STRAND	336	338
FT	STRAND	343	345
FT	STRAND	347	350
FT	TURN	355	356
FT	STRAND	360	363
FT	HELIX	365	368
FT	TURN	369	370
FT	STRAND	371	376
FT	TURN	377	380
FT	STRAND	381	388
SQ	SEQUENCE	388 AA;	42426 MW; F862DFDC1438BB92 CRC64;

Query Match 13.1%; Score 353; DB 1; Length 388;
 Best Local Similarity 29.1%; Pred. No. 2.7e-18;
 Matches 120; Conservative 65; Mismatches 120; Indels 108; Gaps 21;

Qy	52	PAERHADG-LALALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVD	110
		:: :: : : : : :	
Db	50	PAWKYRFGDLSVTYEP-----MAYMD-----AAYFGEISIGTPPQNFLVLFD	91
Qy	111	TGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFVGEDL	162
		: : : :	
Db	92	TGSSNLWVPSVYCQSQACTSHS----RFPNSESSTYSTNGQTFSLQYGSGSLTGFFGYDT	147
Qy	163	VTIPKGFNTSFLVNIATIFESENFFLPG----IKWNGILGLAYATLAKPSSSLETFFDS	217
		: : : : : :	
Db	148	LTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMGLAYPALSVDEAT--TAMQG	198
Qy	218	LVTQANI PN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQI	276
		: : : : : : : : :	

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Db      199 MVQEGALTSPVFSVYLSNQ-----QGSSGGAVVFGGVDSSLYTGQIYWAPVTQELYWQI 252
Qy      277 EILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFD AVEAVARASLIPEFSDGF 336
        | : |||: | | :|||:|:| | :|: |::|
Db      253 GIEEFLIGGQASGW-CSE--GCQAIVDTGTSLLTVPQQYMSALLQA----- 295
Qy      337 WTGSQLACWTNSETPWSYF-----PKISYLRDENSSRSFRITILPQLYIQPMMG 386
        ||:| | : | | : : : : | | |
Db      296 -TGAQ-----EDEYGQFLVNCNSIQNLPSLTFII-----NGVEFPLPPSSYI----- 336
Qy      387 AGLNYECY-RFGISP----STNA---LVIGATVMEGFYVIFDRAQKRVGF AAS 431
        |: | |: | | : : | : : | :| | | :
Db      337 --LSNNGYCTVGVEPTYLSSQNGQPLWILGDVFLRSYYSVYDLGNNRVGFATA 387

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RESULT 7

PEPC_CALJA

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ID      PEPC_CALJA      STANDARD;      PRT;      388 AA.
AC      Q9N2D3;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
GN      PGC.
OS      Callithrix jacchus (Common marmoset).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC      Callithrix.
OX      NCBI_TaxID=9483;
RN      [1]
RP      SEQUENCE FROM N.A., SEQUENCE OF 17-26, FUNCTION, AND ENZYME
RP      REGULATION.
RC      TISSUE=Gastric mucosa;
RX      MEDLINE=20250834; PubMed=10788784;
RA      Kageyama T.;
RT      "New World monkey pepsinogens A and C, and prochymosins. Purification,
RT      characterization of enzymatic properties, cDNA cloning, and molecular
RT      evolution.";
RL      J. Biochem. 127:761-770(2000).
CC      -!- FUNCTION: Hydrolyzes a variety of proteins.
CC      -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
CC      shows preferential cleavage at Tyr|-Xaa bonds; high activity
CC      towards hemoglobin as substrate.
CC      -!- ENZYME REGULATION: Inhibited by pepstatin.
CC      -!- MISCELLANEOUS: The optimal pH is around 2.
CC      -!- SIMILARITY: Belongs to peptidase family A1.
CC      -----
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB038385; BAA90872.1; -.
DR      PIR; JC7246; JC7246.

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DR HSSP; P20142; 1AVF.
 DR MEROPS; A01.003; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 59 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 60 388 GASTRICIN.
 FT ACT_SITE 91 91 BY SIMILARITY.
 FT ACT_SITE 276 276 BY SIMILARITY.
 FT DISULFID 104 109 BY SIMILARITY.
 FT DISULFID 267 271 BY SIMILARITY.
 FT DISULFID 310 343 BY SIMILARITY.
 SQ SEQUENCE 388 AA; 42503 MW; 0BC48DBD1F7D2D8C CRC64;

Query Match 13.1%; Score 351.5; DB 1; Length 388;
 Best Local Similarity 30.1%; Pred. No. 3.5e-18;
 Matches 112; Conservative 56; Mismatches 115; Indels 89; Gaps 17;

Qy 92 YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGF 143
 | : | : | | | | | : | | | | | | | | | : | | | | |
 Db 73 YFGEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHS----RFNPSASSTYSSNGQ 128

 Qy 144 DVTVKYQTQGSWTGFVGEDLVTPKGFNTSFLVNIATIFESENFFLPG-----IKWNGILG 198
 : : : | | | | | | : : : | | | | | : : : | : |
 Db 129 TFSLQYGGSLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG 181

 Qy 199 LAYATLAKPSSSLETFFDSLVTQANIPN-VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPS 257
 | | | | : : : | : : : : | | : | : | : : | : |
 Db 182 LAYPALSMGGAT--TAMQGMQLQEGALTSPVFSFYLSNQ-----QGSSGGAVIFGGVDSS 233

 Qy 258 LYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFD 317
 | | | | : : | : : | : | | : | | : | | : | : | : | : | : |
 Db 234 LYTGQIYWAPVTQELYWQIGIEEFLIGGQASGW-CSE--GCQAIVDTGTSLTVPQQYMS 290

 Qy 318 AVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYF-----PKISIIYLRDENS 367
 | : | | | | | | : | | : | | : | : :
 Db 291 AFLEA-----TGAQ-----EDEYQGFLVNCDSIQNLPTLTFFII----- 323

 Qy 368 SRSFRITILPQLYIQPMMGAGLNYECY-RFGISP-----STNALVIGATVMEGFYVIF 419
 : | | | : | | : | | : | : | : | : | : | : | : | : |
 Db 324 -NGVEFPLPPSSYI-----LSNNGYCTVGVEPTYLSSQNSQPLWILGDVFLRSYYSVF 375

 Qy 420 DRAQKRVGFAAS 431
 | | | | :
 Db 376 DLGNNRVGFATA 387

RESULT 8

PEPC_CAVPO

ID PEPC_CAVPO STANDARD; PRT; 394 AA.

AC Q64411;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
 GN PGC.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92355614; PubMed=1644829;
 RA Kageyama T., Ichinose M., Tsukada S., Miki K., Kurokawa K., Koiwai O.,
 RA Tanji M., Yakabe E., Athauda S.B., Takahashi K.;
 RT "Gastric procathepsin E and progastricsin from guinea pig.
 RT Purification, molecular cloning of cDNAs, and characterization of
 RT enzymatic properties, with special reference to procathepsin E.";
 RL J. Biol. Chem. 267:16450-16459(1992).
 CC -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
 CC shows preferential cleavage at Tyr|-Xaa bonds; high activity
 CC towards hemoglobin as substrate.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; M88652; AAA37053.1; -.
 DR PIR; B43356; B43356.
 DR HSSP; P20142; LAVF.
 DR MEROPS; A01.003; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 65 ACTIVATION PEPTIDE.
 FT CHAIN 66 394 GASTRICSIN.
 FT ACT_SITE 97 97 BY SIMILARITY.
 FT ACT_SITE 283 283 BY SIMILARITY.
 FT DISULFID 110 115 BY SIMILARITY.
 FT DISULFID 273 277 BY SIMILARITY.
 FT DISULFID 316 349 BY SIMILARITY.
 SQ SEQUENCE 394 AA; 42995 MW; 114F08E105D49865 CRC64;

Query Match 12.1%; Score 324.5; DB 1; Length 394;
 Best Local Similarity 29.0%; Pred. No. 3.2e-16;
 Matches 107; Conservative 63; Mismatches 116; Indels 83; Gaps 18;

Qy 92 YYLEMLIGTPPQKLQILVDTGSSNF-----AVAGTPHSYIDTYFDTERSSSTYRSKGF 143
 |: :: :|||| | :| ||||| ::| | | | : |||| :

Db 79 YFGQISLGTTPQSFQVLFDTGSSNLWVPSVYCSSLACTTH----TRFNPRDSSTYVATDQ 134

Qy 144 DVTVKYTQGSWTGFVGEDLVTI-----PK-GFNTSFLVNIATIFESENFFLPG-----IK 192
 :::| || || | | :|| || | | | :| || :

Db 135 SFSLEYGTGSLTGFGYDTMTIQDIQVPKQEFGLS-----ETE----PGSDFVYAE 181

Qy 193 WNGILGLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGS--GTNGGSL 249
 :||| || | |:: :: | | : : : :||: : || |:: ||

Db 182 FDGILGLGYPGLSEGGAT--TAMQGLLREGALSQSLFSVYL-----GSQQGSDEGQL 231

Qy 250 VLGgiePSLYKGDWYTPiKEEWYyQIEILKLEIGGQSLNLDcreYNADKAIVDSGTTLL 309
 :||:: || | ||: ||: :| | :| | | | : | : ||: ||: ||

Db 232 ILGGVDESlyTGDIYWTPVTQELyWQIGIEGFLIDGSASGWCSR--GCQGIVDTGTSLL 288

Qy 310 RLPQKVFDaVVEaVaRaSLiPEfSDGfWtGSQlAcWtNsetPwSyfPKiSiYlRdENSSR 369
 :| :|: | : : | :| : : | | :

Db 289 TVPSDYLSTLVQAIGAEe--NEyGEyF-----VSCSSIQDLPTLTfViSGV----- 332

Qy 370 SFRITILPQLYIQP-----MMGAGLNYECYRFGISpSTN--ALVIGATVMegfYViFDRA 422
 : | || | :| | :|| :| : :| :| |

Db 333 --EFPLSPsAYILSGENyCMVGLESTY-----VSPGGGEPVWILGDVFLRSYYSVYDLA 384

Qy 423 QKRVGFaAS 431
 |||| :

Db 385 NNRVGFATA 393

RESULT 9

RENI_MOUSE

ID RENI_MOUSE STANDARD; PRT; 402 AA.

AC P06281; P97911; Q62153; Q62154;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Renin 1 precursor (EC 3.4.23.15) (Angiotensinogenase) (Kidney renin).

GN REN1 OR REN-1 OR REN.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RX MEDLINE=84182525; PubMed=6370686;

RA Holm I., Ollo R., Panthier J.-J., Rougeon F.;

RT "Evolution of aspartyl proteases by gene duplication: the mouse renin gene is organized in two homologous clusters of four exons.";

RL EMBO J. 3:557-562(1984).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c; TISSUE=Kidney;

RX MEDLINE=90067953; PubMed=2685761;

RA Kim W.S., Murakami K., Nakayama K.;

RT "Nucleotide sequence of a cDNA coding for mouse Ren1 preprorenin.";

RL Nucleic Acids Res. 17:9480-9480(1989).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=DBA/2, and C57BL/10;
 RX MEDLINE=90108722; PubMed=2691339;
 RA Burt D.W., Mullins L.J., George H., Smith G., Brooks J., Pioli D.,
 RA Brammar W.J.;
 RT "The nucleotide sequence of a mouse renin-encoding gene, Ren-1d, and
 RT its upstream region.";
 RL Gene 84:91-104(1989).
 RN [4]
 RP SEQUENCE OF 1-30 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=84298161; PubMed=6089205;
 RA Panthier J.-J., Dreyfus M., Roux D.T.L., Rougeon F.;
 RT "Mouse kidney and submaxillary gland renin genes differ in their 5'
 RT putative regulatory sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5489-5493(1984).
 RN [5]
 RP SEQUENCE OF 1-31 FROM N.A.
 RX MEDLINE=85085936; PubMed=6392850;
 RA Field L.J., Philbrick W.M., Howles P.N., Dickinson D.P.,
 RA McGowan R.A., Gross K.W.;
 RT "Expression of tissue-specific Ren-1 and Ren-2 genes of mice:
 RT comparative analysis of 5'-proximal flanking regions.";
 RL Mol. Cell. Biol. 4:2321-2331(1984).
 RN [6]
 RP SEQUENCE OF 22-37 AND 72-80.
 RC STRAIN=C57BL/10ROS X C3H/HEROS; TISSUE=Kidney;
 RX MEDLINE=97182599; PubMed=9030738;
 RA Jones C.A., Petrovic N., Novak E.K., Swank R.T., Sigmund C.D.,
 RA Gross K.W.;
 RT "Biosynthesis of renin in mouse kidney tumor As4.1 cells.";
 RL Eur. J. Biochem. 243:181-190(1997).
 CC -!- FUNCTION: Renin is a highly specific endopeptidase, whose only
 CC known function is to generate angiotensin I from angiotensinogen
 CC in the plasma, initiating a cascade of reactions that produce an
 CC elevation of blood pressure and increased sodium retention by the
 CC kidney.
 CC -!- CATALYTIC ACTIVITY: Cleaves Leu-|- bond in angiotensinogen to
 CC generate angiotensin I.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Kidney.
 CC -!- INDUCTION: Renal renin is synthesized by the juxtaglomerular cells
 CC of the kidney in response to decreased blood pressure and sodium
 CC concentration.
 CC -!- POLYMORPHISM: In inbred mouse strains, there are at least two
 CC alleles which can occur at the Ren1 locus: Ren-1D and Ren-1C.
 CC The sequence shown is that of Ren-1C.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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 CC -----
 DR EMBL; X00810; CAA25391.1; -.

DR EMBL; X00811; CAA25391.1; JOINED.
 DR EMBL; X00812; CAA25391.1; JOINED.
 DR EMBL; X00813; CAA25391.1; JOINED.
 DR EMBL; X00814; CAA25391.1; JOINED.
 DR EMBL; X00815; CAA25391.1; JOINED.
 DR EMBL; X00816; CAA25391.1; JOINED.
 DR EMBL; X00850; CAA25391.1; JOINED.
 DR EMBL; X00851; CAA25391.1; JOINED.
 DR EMBL; X16642; CAA34636.1; -.
 DR EMBL; K02596; AAA40045.1; -.
 DR EMBL; M32352; AAA40043.1; -.
 DR EMBL; K02800; AAA40044.1; -.
 DR EMBL; M34190; AAA40042.1; -.
 DR PIR; A00989; REMSK.
 DR HSSP; P00796; 1SMR.
 DR MEROPS; A01.007; -.
 DR MGD; MGI:97898; Ren1.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Plasma; Glycoprotein; Zymogen;
 KW Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 71 ACTIVATION PEPTIDE.
 FT CHAIN 72 402 RENIN 1.
 FT ACT_SITE 102 102 BY SIMILARITY.
 FT ACT_SITE 287 287 BY SIMILARITY.
 FT DISULFID 115 122 BY SIMILARITY.
 FT DISULFID 278 282 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 58 58 W -> R (in Ren-1D).
 FT VARIANT 68 68 T -> I (in Ren-1D).
 FT VARIANT 160 160 S -> V (in Ren-1D).
 FT VARIANT 315 315 E -> D (in Ren-1D).
 FT VARIANT 352 352 N -> Y (in Ren-1D).
 FT CONFLICT 6 23 MISSING (IN REF. 1).
 FT CONFLICT 24 24 T -> I (IN REF. 1).
 FT CONFLICT 163 163 V -> VSRV (IN REF. 1).
 SQ SEQUENCE 402 AA; 44342 MW; D42920B555E97A38 CRC64;

Query Match 11.9%; Score 320; DB 1; Length 402;
 Best Local Similarity 28.6%; Pred. No. 7e-16;
 Matches 126; Conservative 66; Mismatches 181; Indels 68; Gaps 21;

Qy 10 LPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPG-PGTPAERHADGLALALE--- 65
 :|| | || :| |:| | | : | || | |:|
 Db 6 MPLWALLLL-----WSPCTFSLPTRTATFERIPLKKMPVREILEERGVDMLRLSAEWGV 60
 Qy 66 ----PA---LASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAV 118
 |: | || |:| | | || |: ||||| :: ||||:| |
 Db 61 FTKRPSLTNLTSPVVLTNYL-----NTQ-----YYGEIGIGTPPQTFKVFIDTGSANLWV 110

Qy 119 AGTPHSY-----IDTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLV TIPKGFNTS 172
 | | : :: ||:| | | : | | ||: :| ||: | :
 Db 111 PSTKCSRLYLACGIHSLYESSDSSSYMENGSDFTTIHYGSGRVKGFLSQDSVTV-GGITVT 169

Qy 173 FLVNIATIFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQ 231
 | | | :||:| | : | : | | : :| | : ||:
 Db 170 QTFGEVTELPLIPFML--AKFDGVLGMGFP--AQAVGGVTPVFDHILSQGV LKEEVFSVY 225

Qy 232 MCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD 291
 || || :||| :| | :| | | : :|| : : :| | |
 Db 226 Y-----NRGSHLLGGEVVLGGSDPQHYQGNFHYVSISKTD SWQITMKGVS VG--SSTLL 277

Qy 292 CREYNADKAIVDSGTTLLRLPQKVFDAVVEAV-ARASLIPEFS DGFWTGSQ LACWTNSET 350
 | | | :||:| : : | : :||: | : | | : : | | :
 Db 278 CEEGCA--VVVDTGSSSFISAPTSSLKLIMQALGAKEKRIEY-----VVNC---SQV 324

Qy 351 PWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGL-NYECYRFGISPSTNAL-VIG 408
 | | || | | : : : : | : | : | | : | :|
 Db 325 P--TLPDISFDL----GGRAYTLSS TDYVLQYPNRRDKLCT LALHAMDIPPTGPVWVLG 378

Qy 409 ATVMEGFYVIFDRAQKRVGFA 429
 || : || || | :|||
 Db 379 ATFIRKFYTEFDRHNNRIGFA 399

RESULT 10

CATD_CLUHA

ID CATD_CLUHA STANDARD; PRT; 396 AA.
 AC Q9DEX3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cathepsin D precursor (EC 3.4.23.5).
 OS Clupea harengus (Atlantic herring).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
 OC Clupea.
 OX NCBI_TaxID=7950;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nielsen L.B., Stougaard P., Andersen P.S., Pedersen L.H.;
 RT "Cloning and sequence determination of herring muscle cathepsin D.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 62-82.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=21165469; PubMed=11207447;
 RA Nielsen L.B., Nielsen H.H.;
 RT "Purification and characterization of cathepsin D from herring muscle
 (Clupea harengus).";
 RL Comp. Biochem. Physiol. 128B:351-363(2001).
 CC -!- FUNCTION: Cathepsin D is an acid protease active in intracellular
 CC protein breakdown.
 CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
 CC that of pepsin A. Does not cleave the 4-Gln-|-His-5 bond in B
 CC chain of insulin.
 CC -!- ENZYME REGULATION: Inhibited by pepstatin.


```

      |::| : : || | | | |:: :|||:|::| : | ::: ||
Db      255 YWQIHMDGMSIGSQ-LTL-CKD--GCEAIVDTGTSLITGPPAEVRALQKAIGAIPLIQGE 310
Qy      330 -----PEFSDGFWTGSQ LACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQ 378
      | | | | : | | | | ::: :: :: |
Db      311 YMIDCKKVPTLPTIS--FNVGGK----TYSLTGEQY-----VLKESQGGKTICLSGLMG 358
Qy      379 LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAAS 431
      | | | : : : : | :|| | |||| |
Db      359 LEIPP-----PAGPLWILGDVFIGQYYTVFDRESNRVGFAS 395

```

RESULT 11

APR1_ORYSA

ID APR1_ORYSA STANDARD; PRT; 509 AA.

AC Q42456;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Aspartic proteinase oryzasin 1 precursor (EC 3.4.23.-).

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare / Japonica; TISSUE=Seed;

RX MEDLINE=96048031; PubMed=7556174;

RA Asakura T., Watanabe H., Abe K., Arai S.;

RT "Rice aspartic proteinase, oryzasin, expressed during seed ripening

RT and germination, has a gene organization distinct from those of

RT animal and microbial aspartic proteinases.";

RL Eur. J. Biochem. 232:77-83(1995).

CC -!- DEVELOPMENTAL STAGE: Seed ripening and germination.

CC -!- SIMILARITY: Belongs to peptidase family A1.

CC

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CC

DR EMBL; D32165; BAA06876.1; -.

DR EMBL; D32144; BAA06875.1; -.

DR PIR; S66516; S66516.

DR HSSP; P42210; 1QDM.

DR MEROPS; A01.020; -.

DR Gramene; Q42456; -.

DR InterPro; IPR001969; Aspprotease_AS.

DR InterPro; IPR009007; Pept_A_acid.

DR InterPro; IPR001461; Peptidase_A1.

DR InterPro; IPR007856; SapB_1.

DR InterPro; IPR008138; SapB_2.

DR InterPro; IPR008140; SapB_sub.


```

Qy      337 -----WTGSQLACWTNSETPSY-----FPKISYLRD 364
          | :||| : :|          |:|| :
Db      384 NACEMAVVWMQNQLAQNKTDLILNYINQLCDKLPSPMGESSVDCGSLASMPETISFTIGA 443

Qy      365 ENSSRSFRITILPQLYIQPMMGAGLNYECY---RFGISPSTNAL-VIGATVMEGFYVIF 419
          : : : |:|| :| | :| | | | :| | : : :|
Db      444 K-----KFALKPEEYIL-KVGEAAQACISGFTAMDIPPRGPLWILGDVFMGAYHTVF 496

Qy      420 DRAQKRVGFAAS 431
          | : ||||| |
Db      497 DYGKMVRVGFAKS 508

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RESULT 12

PEPC RAT

```

ID      PEPC_RAT          STANDARD;      PRT;      392 AA.
AC      P04073;
DT      01-NOV-1986 (Rel. 03, Created)
DT      01-NOV-1986 (Rel. 03, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Gastricsin precursor (EC 3.4.23.3) (Pepsinogen C).
GN      PGC.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Wistar;
RX      MEDLINE=89255508; PubMed=2722863;
RA      Ishihara T., Ichihara Y., Hayano T., Katsura I., Sogawa K.,
RA      Fujii-Kuriyama Y., Takahashi K.;
RT      "Primary structure and transcriptional regulation of rat pepsinogen C
RT      gene.";
RL      J. Biol. Chem. 264:10193-10199(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Wistar;
RX      MEDLINE=87054020; PubMed=3780741;
RA      Ichihara Y., Sogawa K., Morohashi K., Fujii-Kuriyama Y., Takahashi K.;
RT      "Nucleotide sequence of a nearly full-length cDNA coding for
RT      pepsinogen of rat gastric mucosa.";
RL      Eur. J. Biochem. 161:7-12(1986).
RN      [3]
RP      SEQUENCE OF 16-112.
RC      STRAIN=Wistar;
RX      MEDLINE=84257697; PubMed=6743670;
RA      Arai K.M., Muto N., Tani S., Akahane K.;
RT      "The N-terminal sequence of rat pepsinogen.";
RL      Biochim. Biophys. Acta 788:256-261(1984).
CC      -!- CATALYTIC ACTIVITY: More restricted specificity than pepsin A, but
CC      shows preferential cleavage at Tyr-Xaa bonds; high activity
CC      towards hemoglobin as substrate.
CC      -!- SIMILARITY: Belongs to peptidase family A1.
-----
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 CC -----

DR EMBL; M25993; AAA41827.1; -.
 DR EMBL; M25985; AAA41827.1; JOINED.
 DR EMBL; M25986; AAA41827.1; JOINED.
 DR EMBL; M25987; AAA41827.1; JOINED.
 DR EMBL; M25988; AAA41827.1; JOINED.
 DR EMBL; M25989; AAA41827.1; JOINED.
 DR EMBL; M25990; AAA41827.1; JOINED.
 DR EMBL; M25991; AAA41827.1; JOINED.
 DR EMBL; M25992; AAA41827.1; JOINED.
 DR EMBL; X04644; CAA28305.1; -.
 DR PIR; A33510; A24608.
 DR HSSP; P20142; 1AVF.
 DR MEROPS; A01.003; -.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Zymogen; Digestion; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 62 ACTIVATION PEPTIDE.
 FT CHAIN 63 392 GASTRICIN.
 FT ACT_SITE 94 94
 FT ACT_SITE 280 280
 FT DISULFID 107 112 BY SIMILARITY.
 FT DISULFID 270 275 BY SIMILARITY.
 FT DISULFID 314 347 BY SIMILARITY.
 FT CONFLICT 31 31 E -> Q (IN REF. 3).
 FT CONFLICT 103 103 S -> A (IN REF. 3).
 FT CONFLICT 109 109 S -> L (IN REF. 3).
 SQ SEQUENCE 392 AA; 42833 MW; 092A5EAF2783EDD1 CRC64;

Query Match 11.6%; Score 313; DB 1; Length 392;
 Best Local Similarity 29.5%; Pred. No. 2.2e-15;
 Matches 105; Conservative 56; Mismatches 139; Indels 56; Gaps 16;

Qy 92 YYLEMLIGTPPQKLQILVDTGSSNFAV-----AGTPHSYIDTYFDTERSSTYRSKGF 143
 |: |: ||||| |: ||||| | | |: |: ||||| ::|
 Db 76 YFGEISIGTPPQNFLVLFDTGSSNLWVSSVYCQSEACTTHA----RFNPSKSSTYYTEGQ 131
 Qy 144 DVTVKYTGGSWTGFVGEDLVITPKGFNTSFLVNIATIFESENFFLPG-----IKWNGILG 198
 :::| || ||| | |:: | | ||| || ::||:|
 Db 132 TFSLQYGTGSLTGFFGYDTLTV-----QSIQVPNQEFGLSEN--EPGTNFVYAQFDGIMG 184
 Qy 199 LAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGS--GTNGGSLVLGGIEP 256
 ||| |: | |::: | : | | || |:||| :| ||::
 Db 185 LAYPGLS---SGGATTALQGMGLGE----GALSQPLFGVYL---GSQQGSNGGQIVFGGVDK 235
 Qy 257 SLYKGDIIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTLLRLPQKVF 316
 :|| |:| : |:| |::| | | | : |||:|:|:| :| :

FT ACT_SITE 276 276 BY SIMILARITY.
 FT DISULFID 107 112 BY SIMILARITY.
 FT DISULFID 267 271 BY SIMILARITY.
 FT DISULFID 310 344 BY SIMILARITY.
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 51 51 T -> S.
 SQ SEQUENCE 383 AA; 41719 MW; 1642796871611F54 CRC64;

Query Match 11.5%; Score 310; DB 1; Length 383;
 Best Local Similarity 26.8%; Pred. No. 3.5e-15;
 Matches 106; Conservative 63; Mismatches 136; Indels 90; Gaps 15;

Qy 56 HA--DGLALALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGS 113
 || || : || | | | | | | | | : ||||| : ||||
 Db 55 HAFPDVLTVVTEPLL-----NTLDM-----EYYGTISIGTPPQDFTVVVFDTS 97

 Qy 114 SNFAVAG----TPHSYIDTYFDTERSSTYRSKGFDTVKYTGGSWTGFVGEDLVITPKGF 169
 || | : | | : ||||| | : : | | | | ||:
 Db 98 SNLWVPSVSCTSPACQSHQMFNPSQSSTYKSTGQNLSTHYGTGDMEGTVGCDTIVTVASLM 157

 Qy 170 NTSFLVNIATIFESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANI-PNVF 228
 : | : | : | | : : ||||| | : | : : |||| : : : | : |
 Db 158 DTNQLFGLST-SEPGQFFV-YVKFDGILGLGYPSLA--ADGITPVFDNMVNESLLEQNLF 213

 Qy 229 SMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSL 288
 | : : : | : | ||| : | : | | : | : | : | : | : | :
 Db 214 SVYLSREPM-----GSMVVFGGIDESYFTGSINWIPVSYQGYWQISMDSIIVNKQEI 265

 Qy 289 NLDCREYNADKAIVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNS 348
 : : ||||| : | : : || |
 Db 266 ACS----SGCQAIIDTGTSLVAGPASDINDIQSAVG-----ANQ 300

 Qy 349 ETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNY-----ECY 394
 | | | | : | : : | | : | : |
 Db 301 NTYGEY-----SVNCSHILAMPDVVF--VIG-GIQYPVPALAYTEQNGQGTCTM 345

 Qy 395 RFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFA 429
 : | : : | : : | |||| ||| |
 Db 346 SSFQNSSADLWILGDVFIIRVYYSIFDRANNRVGLA 380

RESULT 14

CATD_HUMAN

ID CATD_HUMAN STANDARD; PRT; 412 AA.
 AC P07339;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cathepsin D precursor (EC 3.4.23.5).
 GN CTSD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85270436; PubMed=3927292;
 RA Faust P.L., Kornfeld S., Chirgwin J.M.;
 RT "Cloning and sequence analysis of cDNA for human cathepsin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4910-4914(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87231068; PubMed=3588310;
 RA Westley B.R., May F.E.B.;
 RT "Oestrogen regulates cathepsin D mRNA levels in oestrogen responsive
 RT human breast cancer cells.";
 RL Nucleic Acids Res. 15:3773-3786(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91299158; PubMed=2069717;
 RA Redecker B., Heckendorf B., Grosch H.W., Mersmann G., Hasilik A.;
 RT "Molecular organization of the human cathepsin D gene.";
 RL DNA Cell Biol. 10:423-431(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=94085791; PubMed=8262386;
 RA May F.E., Smith D.J., Westley B.R.;
 RT "The human cathepsin D-encoding gene is transcribed from an estrogen-
 RT regulated and a constitutive start point.";
 RL Gene 134:277-282(1993).
 RN [6]
 RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE=95021301; PubMed=7935485;
 RA Augereau P., Miralles F., Cavailles V., Gaudet C., Parker M.,
 RA Rochefort H.;
 RT "Characterization of the proximal estrogen-responsive element of
 RT human cathepsin D gene.";

RL Mol. Endocrinol. 8:693-703(1994).
 RN [7]
 RP SEQUENCE OF 170-180.
 RC TISSUE=Liver;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 RA Appel R.D., Hughes G.J.;
 RL Submitted (JUN-1992) to Swiss-Prot.
 RN [8]
 RP CARBOHYDRATE-LINKAGE SITE ASN-263.
 RX MEDLINE=22660472; PubMed=12754519;
 RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
 RT "Identification and quantification of N-linked glycoproteins using
 RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
 RL Nat. Biotechnol. 21:660-666(2003).
 RN [9]
 RP VARIANT VAL-58.
 RX MEDLINE=20179010; PubMed=10716266;
 RA Papassotiropoulos A., Bagli M., Kurz A., Kornhuber J., Forstl H.,
 RA Maier W., Pauls J., Lautenschlager N., Heun R.;
 RT "A genetic variation of cathepsin D is a major risk factor for
 RT Alzheimer's disease.";
 RL Ann. Neurol. 47:399-403(2000).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 RC TISSUE=Spleen;
 RX MEDLINE=93223670; PubMed=8467789;
 RA Metcalf P., Fusek M.;
 RT "Two crystal structures for cathepsin D: the lysosomal targeting
 RT signal and active site.";
 RL EMBO J. 12:1293-1302(1993).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC TISSUE=Liver;
 RX MEDLINE=93342076; PubMed=8393577;
 RA Baldwin E.T., Bhat T.N., Gulnik S., Hosur M.V., Sowder R.C. II,
 RA Cachau R.E., Collins J., Silva A.M., Erickson J.W.;
 RT "Crystal structures of native and inhibited forms of human cathepsin
 RT D: implications for lysosomal targeting and drug design.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:6796-6800(1993).
 CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
 CC Involved in the pathogenesis of several diseases such as breast
 CC cancer and possibly Alzheimer's disease.
 CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
 CC that of pepsin A. Does not cleave the 4-Gln-|-His-5 bond in B
 CC chain of insulin.
 CC -!- SUBUNIT: Consists of a light chain and a heavy chain.
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- POLYMORPHISM: The Val-58 allele is significantly overrepresented
 CC in demented patients (11.8%) compared with nondemented controls
 CC (4.9%). Carriers of the Val-58 allele have a 3.1-fold increased
 CC risk for developing AD than noncarriers.
 CC -!- SIMILARITY: Belongs to peptidase family A1.
 CC -----
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DR EMBL; M11233; AAB59529.1; -.
 DR EMBL; X05344; CAA28955.1; -.
 DR EMBL; M63138; AAA51922.1; -.
 DR EMBL; M63134; AAA51922.1; JOINED.
 DR EMBL; M63135; AAA51922.1; JOINED.
 DR EMBL; M63136; AAA51922.1; JOINED.
 DR EMBL; M63137; AAA51922.1; JOINED.
 DR EMBL; BC016320; AAH16320.1; -.
 DR EMBL; L12980; AAA16314.1; -.
 DR EMBL; S74689; AAD14156.1; -.
 DR EMBL; S52557; AAD13868.1; -.
 DR PIR; A25771; KHHUD.
 DR PDB; 1LYA; 31-JAN-94.
 DR PDB; 1LYB; 31-JAN-94.
 DR PDB; 1LYW; 22-JUL-99.
 DR MEROPS; A01.009; -.
 DR SWISS-2DPAGE; P07339; HUMAN.
 DR Siena-2DPAGE; P07339; -.
 DR Genew; HGNC:2529; CTSD.
 DR MIM; 116840; -.
 DR GO; GO:0004192; F:cathepsin D activity; TAS.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Signal; Zymogen;
 KW Polymorphism; Alzheimer's disease; 3D-structure.

FT	SIGNAL	1	18	
FT	PROPEP	19	64	ACTIVATION PEPTIDE.
FT	CHAIN	65	412	CATHEPSIN D.
FT	CHAIN	65	161	CATHEPSIN D LIGHT CHAIN (PROBABLE).
FT	CHAIN	169	412	CATHEPSIN D HEAVY CHAIN (PROBABLE).
FT	ACT_SITE	97	97	
FT	ACT_SITE	295	295	
FT	DISULFID	91	160	
FT	DISULFID	110	117	
FT	DISULFID	286	290	
FT	DISULFID	329	366	
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .).
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. . .).
FT	VARIANT	58	58	A -> V (ASSOCIATED WITH INCREASED RISK IN
FT				AD; POSSIBLY INFLUENCES SECRETION AND
FT				INTRACELLULAR MATURATION; dbSNP:17571).
FT				/FTId=VAR_011621.
FT	STRAND	67	74	
FT	TURN	75	77	
FT	STRAND	78	85	
FT	TURN	86	89	
FT	STRAND	90	97	
FT	TURN	98	99	

FT	STRAND	103	107
FT	TURN	108	109
FT	TURN	112	113
FT	HELIX	115	118
FT	TURN	119	119
FT	STRAND	123	123
FT	HELIX	125	127
FT	TURN	129	130
FT	STRAND	132	141
FT	STRAND	146	158
FT	STRAND	172	184
FT	HELIX	188	192
FT	STRAND	197	200
FT	HELIX	204	206
FT	HELIX	208	210
FT	HELIX	214	220
FT	TURN	221	222
FT	STRAND	228	233

Query Match 11.5%; Score 308.5; DB 1; Length 412;
 Best Local Similarity 27.1%; Pred. No. 5e-15;
 Matches 121; Conservative 75; Mismatches 180; Indels 71; Gaps 22;

Qy	9	LLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTPG-----PGTPAERHADGLAL	62
		: : : : : :	
Db	6	LLPLAL--CLLAAP--ASALVRIPLHKFTSIRRTMSEVGGSVEDLIAKGPVSKYSQAVPA	61
Qy	63	ALEPALASPAGAAFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTP	122
		: :	
Db	62	VTEGPI--PEVLKNYM-----DAQYYGEIGIGTPPQCFTVVFDTGSSNLWVPSIH	109
Qy	123	HSYIDT-----YFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVLTIP--KGENTSFL	174
		: : : : :	
Db	110	CKLLDIACWIHHKYNDSKSSYVKNGTSFDIHYGSGSLSGYLSQDTSVSPCQSASSASAL	169
Qy	175	--VNIATIFESENFFLPGI-----KWNIGILGLAYATLAKPSSSLETFFDSLVTQANI-PN	226
		:	
Db	170	GGVKVERQVFGEATKQPGITFIAAKFDGILGMAYPRIS--VNNVLPVFDNLMQQKLVDQN	227
Qy	227	VFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQ	286
		:	
Db	228	IFSFY-----LSRDPDAQPGGELMLGGTDSKYYKGSLSYLNVTWKAYWQVHLDQVEV-AS	281
Qy	287	SLNLDCREYNADKAIVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWT	346
Db	282	GLTL-CKE--GCEAIVDTGTSLMVGP---VDEVRELQKAIGAVPLIQGEY----MIPC--	329
Qy	347	NSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRF---GISPSTN	403
Db	330	---EKVSTLPAITLKL---GGKGYKLS--PEDYTLKVSQAGKTLCLSGFMGMDIPPPSG	380
Qy	404	AL-VIGATVMEGFYVIFDRAQKRVGFA	429
		: : : :	
Db	381	PLWILGDVFIGRYTTFVDRDNNRVGFA	407

RESULT 15

CATD_MOUSE

ID CATD_MOUSE STANDARD; PRT; 410 AA.
AC P18242;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cathepsin D precursor (EC 3.4.23.5).
GN CTSD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=91088345; PubMed=2263503;
RA Diedrich J.F., Staskus K.A., Retzel E.F., Haase A.T.;
RT "Nucleotide sequence of a cDNA encoding mouse cathepsin D.";
RL Nucleic Acids Res. 18:7184-7184(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90326544; PubMed=2374732;
RA Grusby M.J., Mitchell S.C., Glimcher L.H.;
RT "Molecular cloning of mouse cathepsin D.";
RL Nucleic Acids Res. 18:4008-4008(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=94280622; PubMed=8011168;
RA Hetman M., Perschl A., Saftig P., von Figura K., Peters C.;
RT "Mouse cathepsin D gene: molecular organization, characterization of
RT the promoter, and chromosomal localization.";
RL DNA Cell Biol. 13:419-427(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Acid protease active in intracellular protein breakdown.
 CC -!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than,
 CC that of pepsin A. Does not cleave the 4-Gln-|-His-5 bond in B
 CC chain of insulin.
 CC -!- SUBUNIT: Consists of a light chain and a heavy chain.
 CC -!- SUBCELLULAR LOCATION: Lysosomal.
 CC -!- SIMILARITY: Belongs to peptidase family A1.

CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X53337; CAA37423.1; -.
 DR EMBL; X52886; CAA37067.1; -.
 DR EMBL; X68378; CAA48453.1; -.
 DR EMBL; X68379; CAA48453.1; JOINED.
 DR EMBL; X68380; CAA48453.1; JOINED.
 DR EMBL; X68381; CAA48453.1; JOINED.
 DR EMBL; X68382; CAA48453.1; JOINED.
 DR EMBL; X68383; CAA48453.1; JOINED.
 DR EMBL; BC054758; AAH54758.1; -.
 DR EMBL; BC057931; AAH57931.1; -.
 DR PIR; I48278; KHMSD.
 DR HSSP; P07339; 1LYB.
 DR MEROPS; A01.009; -.
 DR MGD; MGI:88562; Ctsd.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Hydrolase; Aspartyl protease; Glycoprotein; Lysosome; Zymogen; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 64 ACTIVATION PEPTIDE (POTENTIAL).
 FT CHAIN 65 410 CATHEPSIN D.
 FT ACT_SITE 97 97 BY SIMILARITY.
 FT ACT_SITE 293 293 BY SIMILARITY.
 FT DISULFID 91 160 BY SIMILARITY.
 FT DISULFID 110 117 BY SIMILARITY.
 FT DISULFID 284 288 BY SIMILARITY.
 FT DISULFID 327 364 BY SIMILARITY.
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 SQ SEQUENCE 410 AA; 44954 MW; DC4928EC46928BF0 CRC64;

Query Match 11.4%; Score 306.5; DB 1; Length 410;
 Best Local Similarity 27.5%; Pred. No. 6.9e-15;
 Matches 103; Conservative 64; Mismatches 123; Indels 85; Gaps 15;

Qy 92 YYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDT-----YFDTERSSTYRSKGFVDV 145
 || :: ||| ||| :: ||| || | :| :::: ||| |
 Db 79 YYGDIGIGTPPQCFTVVFDTGSSNLWVPSIHCKILDIAWVHHKYNSDKSSTYVKNGTSF 138

Qy 146 TVKYTQGSWTGFVGEDLV TIPKGENTSFLVNIAT---IFESENFFLPGI-----KWNIGIL 197
: | || :|:: :| |::| : | | | | | | :|::|||
Db 139 DIHYGSGSLSGYLSQD TVSVPCCKSDQSKARGIKVEKQIF-GEATKQPGIVFVAAKFDGIL 197

Qy 198 GLAYATLAKPSSSLETFFDSLVTQANI-PNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEP 256
|: | :: :: |::| : |::| | | | | | | :
Db 198 GMGYPHIS--VNNVLPVFDNLMQQKLVDKNIFS FY-----LNRDPEGQPGGELMLGGTDS 250

Qy 257 SLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAI VDSGTTLLRLPQKVF 316
| |:: | : : |:: : : ||:| : | | | : : |||:|:| | :
Db 251 KYYHGELSYLNVTRKAYWQVHMDQLEVGNE-LTL-CK--GGCEAIVDTGTSLLVGPVEEV 306

Qy 317 DAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYLRDENS SRFRITIL 376
: :|: || : | : : : |
Db 307 KELQKAIGAVPLI-----QGEYMIPCEKVSSL 333

Qy 377 PQLYIQPMMGAGLNYEC----YREFGIS-----PSTNALVIGATVMEG 414
| :|:: :| | || | :| | | :| :
Db 334 PTVYLK--LG-GKNYELHPDKYILKVSQGGKTICLSGFMGMDIPPPSGPLWILGDVFIGS 390

Qy 415 FYVIFDRAQKRVGFA 429
:| :||| ||||
Db 391 YYTVFDRDNNRVGFA 405

Search completed: February 28, 2004, 09:09:47

Job time : 13.7727 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 28, 2004, 09:05:15 ; Search time 41.4848 Seconds
(without alignments)
3939.714 Million cell updates/sec

Title: US-09-668-314C-2
Perfect score: 2687
Sequence: 1 MGALARALLPLLAQWLLRA.....RPRDPEVVNDESSLVRHRWK 518

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	2405	89.5	514	11	Q8C5E9	Q8c5e9 mus musculu
2	2399	89.3	514	11	Q8C793	Q8c793 mus musculu
3	2395	89.1	514	11	Q9JL18	Q9jl18 mus musculu
4	2375	88.4	468	4	Q9NZL2	Q9nzl2 homo sapien
5	2293	85.3	439	4	Q9H2V8	Q9h2v8 homo sapien
6	2184	81.3	423	4	Q8N2D4	Q8n2d4 homo sapien
7	1966	73.2	396	4	Q9NZL1	Q9nzl1 homo sapien
8	1693	63.0	500	13	Q7T0Y2	Q7t0y2 xenopus lae
9	1246	46.4	255	11	Q9R1P7	Q9rlp7 mus musculu
10	1186	44.1	501	11	Q8C7R1	Q8c7r1 mus musculu
11	1183.5	44.0	532	4	Q9ULS1	Q9uls1 homo sapien
12	1183	44.0	501	11	Q8BQY4	Q8bqy4 mus musculu
13	1172.5	43.6	501	4	Q8IYC8	Q8iyc8 homo sapien
14	1049	39.0	467	11	Q8C4F4	Q8c4f4 mus musculu
15	653	24.3	267	11	Q9CUU5	Q9cuu5 mus musculu
16	461	17.2	213	4	Q9P0D2	Q9p0d2 homo sapien
17	386	14.4	244	5	Q8WQY9	Q8wqy9 aphrocallis
18	367.5	13.7	383	13	Q9DEC3	Q9dec3 xenopus lae
19	361.5	13.5	389	6	Q9GMY4	Q9gmy4 sorex ungui
20	355.5	13.2	384	13	Q91322	Q91322 rana catesb
21	355	13.2	389	13	Q9W643	Q9w643 gallus gall
22	355	13.2	389	13	Q9PWK1	Q9pwk1 gallus gall
23	351.5	13.1	389	6	Q9GMY3	Q9gmy3 rhinolophus
24	351.5	13.1	389	6	Q9GMY5	Q9gmy5 suncus muri
25	335.5	12.5	388	6	Q9GMY2	Q9gmy2 oryctolagus
26	334.5	12.4	391	5	Q9VKP6	Q9vkp6 drosophila
27	326	12.1	399	13	Q93458	Q93458 podarcis si
28	324.5	12.1	372	5	Q9VLK3	Q9vlk3 drosophila
29	324.5	12.1	383	13	Q9DE45	Q9de45 salvelinus
30	322.5	12.0	390	6	Q8SQ41	Q8sq41 canis famil
31	322.5	12.0	397	13	Q9W6D4	Q9w6d4 hynobius le
32	320	11.9	385	13	Q9DEC4	Q9dec4 rana catesb
33	319.5	11.9	387	13	Q9DDV5	Q9ddv5 salvelinus
34	319	11.9	419	5	Q95VA2	Q95va2 clonorchis
35	318.5	11.9	396	13	Q93428	Q93428 chionodraco
36	318	11.8	397	13	Q800A0	Q800a0 rana catesb
37	316	11.8	378	13	Q9PUR9	Q9pur9 pseudopleur
38	316	11.8	392	11	Q9D7R7	Q9d7r7 mus musculu
39	313	11.6	383	5	O76856	O76856 dictyosteli
40	312.5	11.6	354	5	Q9GYX7	Q9gyx7 boophilus m
41	305	11.4	384	13	Q9DEC2	Q9dec2 xenopus lae
42	302	11.2	398	13	P87370	P87370 oncorhynch
43	301.5	11.2	401	11	Q91X66	Q91x66 mus musculu
44	300.5	11.2	386	6	Q9BGU5	Q9bgu5 bos taurus
45	295.5	11.0	390	6	Q9GK10	Q9gk10 camelus dro

ALIGNMENTS

RESULT 1

Q8C5E9

ID Q8C5E9 PRELIMINARY; PRT; 514 AA.

AC Q8C5E9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Beta-site APP-cleaving enzyme 2.
GN BACE2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK078770; BAC37384.1; -.
DR MGD; MGI:1860440; Bace2.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001969; Aspprotease_AS.
DR InterPro; IPR001461; Peptidase_A1.
DR InterPro; IPR009007; Pept_A_acid.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 2.
SQ SEQUENCE 514 AA; 55811 MW; CBB9237BB68A0B2E CRC64;

Query Match 89.5%; Score 2405; DB 11; Length 514;
Best Local Similarity 88.8%; Pred. No. 3.5e-179;
Matches 460; Conservative 20; Mismatches 34; Indels 4; Gaps 1;

Qy 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGL 60
| | | | | : | | | | | : | | | | | : | | | | |
Db 1 MGALLRALLLPVLAQWLLSAVPALAPAPFTLPLQVARATNHRASAVPGLGTPGLPRADGL 60

Qy 61 ALALEPALASPAGAAFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
| | | | | : | | | | | : | | | | | : | | | | |
Db 61 ALALEPVVRAT----ANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKVQILVDTGSSNFAVAG 116

Qy 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 180
| | | | | : | | | | | : | | | | | : | | | | |
Db 117 APHSYIDTYFDSESSSTYHSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATI 176

Qy 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
| | | | | : | | | | | : | | | | | : | | | | |
Db 177 FESENFLLPGIKWNGILGLAYAALAKPSSSLETFFDSLVAQAKIPDIFSMQMCAGLPVA 236

Qy 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300
| | | | | : | | | | | : | | | | | : | | | | |
Db 237 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 296

Qy 301 IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
| | | | | : | | | | | : | | | | | : | | | | |
Db 297 IVDSGTTLLRLPQKVFDVAVVEAVARTSLIPEFSDGFWTGAQLACWTNSETPWAYFPKISI 356

Qy 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
| | | | | : | | | | | : | | | | | : | | | | |

Db 357 YLRDENASRSFRITILPQLYIQPMGAGFNYECYRFGISSSTNALVIGATVMEGFYVVF 416

Qy 421 RAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
 |||:|||| | ||| |||||:|||||:|:|||||

Db 417 RAQRRVGFAVSPCAEIEGTTVSEISGPFSTEDIASNCVPAQALNEPILWIVSYALMSVCG 476

Qy 481 AILLVLIVLLLLPFRQRRPRDPEVVNDESSLVRHRWK 518
 |||||:|||| |: |||||

Db 477 AILLVLIVLLLLPLHCRHAPRDPEVVNDESSLVRHRWK 514

RESULT 2

Q8C793

ID Q8C793 PRELIMINARY; PRT; 514 AA.

AC Q8C793;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Beta-site APP-cleaving enzyme 2.

GN BACE2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Heart;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

DR EMBL; AK052309; BAC34931.1; -.

DR MGD; MGI:1860440; Bace2.

DR GO; GO:0004194; F:pepsin A activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR001969; Aspprotease_AS.

DR InterPro; IPR001461; Peptidase_A1.

DR InterPro; IPR009007; Pept_A_acid.

DR Pfam; PF00026; asp; 1.

DR PRINTS; PR00792; PEPSIN.

DR PROSITE; PS00141; ASP_PROTEASE; 2.

SQ SEQUENCE 514 AA; 55871 MW; 8BF45E07B0990225 CRC64;

Query Match 89.3%; Score 2399; DB 11; Length 514;

Best Local Similarity 88.6%; Pred. No. 1e-178;

Matches 459; Conservative 20; Mismatches 35; Indels 4; Gaps 1;

Qy 1 MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGL 60
 |||| |||||:|||| | | |||||:| ||| : || ||| ||||

Db 1 MGALLRALLLPVLAQWLLSAVPALAPAPFTLPLQVARATNHRASAVPGLGTPELPRADGL 60

Qy 61 ALALEPALASPAGAAANFLAMVDNLQGD SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG 120
 ||||| |: |||||

Db 61 ALALEPVRAT----ANFLAMVDNLQGD SGRGYYLEMLIGTPPQKVQILVDTGSSNFAVAG 116

QY 121 TPHSYIDTYFDTERSSTYRSKGFDTVKYTGQSWTGFVGEDLVITIPKGFNTSFLVNIATI 180
 |||||:| ||| |||||:|||||
 Db 117 APHSYIDTYFDSESSSTYHSGKGFDTVKYTGQSWTGFVGEDLVITIPKGFNTSFLVNIATI 176

QY 181 FESENFLLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA 240
 |||||:| ||| |||||:| |||:| |||||
 Db 177 FESENFLLPGIKWNGILGLAYAAALAKPSSSLETFFDSLVAQAKIPDIFSMQMCGAGLPVA 236

QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 300
 |||||:| ||| |||||:| |||||
 Db 237 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKA 296

QY 301 IVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
 |||||:| ||| |||||:| |||||:| |||||
 Db 297 IVDSGTTLLRLPQKVFDAVVEAVARTSLIPEFSDGFWTGAQLACWTNSETPWAYFPKISI 356

QY 361 YLRDENSSRSFRITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 420
 |||||:| ||| |||||:| |||||:| |||||:| |||||
 Db 357 YLRDENASRSFRITILPQLYIQPMGAGLNYECYRFGISSSTNALVIGATVMEGFYVIFD 416

QY 421 RAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCG 480
 |||:| ||| ||||| | |||||:| |||||:| |||||:| |||||
 Db 417 RAQRRVGFAVSPCAIEGTTVSEISGPFSTEDIASNCVPAQALNEPIWIVSYALMSVCG 476

QY 481 AILLVLIVLLLLLPRCQRRPRDPEVVNDESSLVRHRWK 518
 |||||:| ||| | : |||||
 Db 477 AILLVLIVLLLLLPLHCRHAPRDPEVVNDESSLVRHRWK 514

RESULT 3

Q9JL18

ID Q9JL18 PRELIMINARY; PRT; 514 AA.
 AC Q9JL18;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aspartyl protease 1.
 GN BACE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Choi D.K., Sugano S., Sakaki Y.;
 RT "Molecular characterization of the mouse Aspl gene, a homolog of the
 RT human ASP1 (Down Syndrome Region aspartyl protease).";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR EMBL; AF216310; AAF36599.1; -.
 DR HSSP; P00797; 2REN.
 DR MEROPS; A01.041; -.
 DR MGD; MGI:1860440; Bace2.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.

GN BACE2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20422477; PubMed=10965118;
 RA Solans A., Estivill X., de La Luna S.;
 RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to
 RT Alzheimer's amyloid precursor protein beta-secretase.";
 RL Cytogenet. Cell Genet. 89:177-184(2000).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR EMBL; AF188276; AAF35835.1; -.
 DR HSSP; P00797; 2REN.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Aspartyl protease; Hydrolase; Protease.
 SQ SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;

Query Match 88.4%; Score 2375; DB 4; Length 468;
 Best Local Similarity 90.3%; Pred. No. 6.6e-177;
 Matches 468; Conservative 0; Mismatches 0; Indels 50; Gaps 1;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGP	TPAERHADGL	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGP	TPAERHADGL	60
Qy	61	ALALEPALASPAGAAFLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAAFLAMVDNLQGD	SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGF	DVTVKYTGQSWTGFGVGEDLVTIPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGF	DVTVKYTGQSWTGFGVGEDLVTIPKGFNTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240	
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240	
Qy	241	GGTGNGGSLVLGGIEPSLYKGDWYTPIKEEWWWQIEILKLEIGGQSLNLD CREYNADKA	300	
Db	241	GGTGNGGSLVLGGIEPSLYKGDWYTPIKEEWWWQIEILKLEIGGQSLNLD CREYNADKA	300	
Qy	301	IVDSGTTLLRLPQKVFD	AVVEAVARASLIPEFSDGFWTGSQ	LACWTNSETPWSYFPKISI 360
Db	301	IVDSGTTLLRLPQKVFD	AVVEAVARASL-----	328
Qy	361	YLRDENSSRSFRITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD	420	

Db 329 -----LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFD 370

Qy 421 RAQKRVGF AASPCA EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 480
 |||

Db 371 RAQKRVGF AASPCA EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCG 430

Qy 481 AILLVLIVLLLLPFR CQRRPRDPEVVNDESSLVRHRWK 518
 |||

Db 431 AILLVLIVLLLLPFR CQRRPRDPEVVNDESSLVRHRWK 468

RESULT 5

Q9H2V8

ID Q9H2V8 PRELIMINARY; PRT; 439 AA.
 AC Q9H2V8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CDA13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pheochromocytoma;
 RA Li Y., Huang Q., Peng, y, Song H., Yu Y., Xu S., Ren S., Chen Z.,
 RA Han Z.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
 DR EMBL; AF212252; AAG41783.1; -.
 DR HSSE; P00797; 2REN.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Aspartyl protease; Hydrolase; Protease.
 SQ SEQUENCE 439 AA; 48275 MW; 02EC0E0E50F11602 CRC64;

Query Match 85.3%; Score 2293; DB 4; Length 439;
 Best Local Similarity 100.0%; Pred. No. 1.5e-170;
 Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 MVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSHYIDTYFDTERSSTYR 139
 |||

Db 1 MVDNLQGDSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSHYIDTYFDTERSSTYR 60

Qy 140 SKGFDVTVKYTQGSWTGFGVGEDLVTPKGFNTSFLVNIATIFESENFFLPGIKWNGLGL 199
 |||

Db 61 SKGFDVTVKYTQGSWTGFGVGEDLVTPKGFNTSFLVNIATIFESENFFLPGIKWNGLGL 120

Qy 200 AYATLAKPSSSLETFFDSIVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLY 259

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      |||||||
Db      121 AYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSIVLGGIEPSLY 180
      |||||||
QY      260 KGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFD AV 319
      |||||||
Db      181 KGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFD AV 240
      |||||||
QY      320 VEA VARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYLRDENSSRSFRITILPQL 379
      |||||||
Db      241 VEA VARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKIS IYLRDENSSRSFRITILPQL 300
      |||||||
QY      380 YIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKR VGFAASPCA EIAGA 439
      |||||||
Db      301 YIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKR VGFAASPCA EIAGA 360
      |||||||
QY      440 AVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCGAILLV LIVLLLLPFR CQRR 499
      |||||||
Db      361 AVSEISGPFSTEDVASNCVPAQSLSEPI LWIVSYALMSVCGAILLV LIVLLLLPFR CQRR 420
      |||||||
QY      500 PRDPEVVNDESSLVRHRWK 518
      |||||||
Db      421 PRDPEVVNDESSLVRHRWK 439

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RESULT 6

Q8N2D4

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ID      Q8N2D4      PRELIMINARY;      PRT;      423 AA.
AC      Q8N2D4;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein OVARC1000363.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Ovarian carcinoma;
RA      Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA      Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA      Nagahari K., Sugano S., Isogai T.;
RT      "HRI human cDNA sequencing project.";
RL      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AK075539; BAC11682.1; -.
DR      GO; GO:0004194; F:pepsin A activity; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR001969; Aspprotease_AS.
DR      InterPro; IPR001461; Peptidase_A1.
DR      InterPro; IPR009007; Pept_A_acid.
DR      Pfam; PF00026; asp; 1.
DR      PRINTS; PR00792; PEPSIN.
DR      PROSITE; PS00141; ASP_PROTEASE; 2.
KW      Hypothetical protein.
SQ      SEQUENCE      423 AA;      46457 MW;      4D4839F2ED9C2CE1 CRC64;

```

Query Match 81.3%; Score 2184; DB 4; Length 423;

Best Local Similarity 99.3%; Pred. No. 4.7e-162;

Matches 420; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy      96 MLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWT 155
      |||
Db      1 MLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVKYTQGSWT 60

Qy     156 GFVGEDLV TIPKG FNTSFLVNIATIFESENFFLPGIKWNGILGLAYATLAKPSSSLETFF 215
      |||
Db      61 GFVGEDLV TIPKG FNTSFLVNIATIFESEGNFFLPGIQWNGILGLAYATLAKPSSSLETFF 120

Qy     216 DSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLGGIEPSLYKGGDIWYTPIKEEWYYQ 275
      |||
Db     121 DSLVTQANIPNVFSMQMRGAGLPVAGSGTNGGSLVLGGIEPSLYKGGDIWYTPIKEEWYYQ 180

Qy     276 IEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDG 335
      |||
Db     181 IEILKLEIGGQSLNLD CREYNADKAIVDSGTTLLRLPQKVFDAVVEAVARASLIPEFSDG 240

Qy     336 FWTGSQLACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNYECYR 395
      |||
Db     241 FWTGSQLACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNYECYR 300

Qy     396 FGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVAS 455
      |||
Db     301 FGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGAAVSEISGPFSTEDVAS 360

Qy     456 NCVPAQSLSEPILWIVSYALMSVCGAILLV LIVLLLLPFR CQRRPRDPEVVNDESSLVRH 515
      |||
Db     361 NCVPAQSLSEPILWIVSYALMSVCGAILLV LIVLLLLPFR CQRRPRDPEVVNDESSLVRH 420

Qy     516 RWK 518
      |||
Db     421 RWK 423
```

RESULT 7

Q9NZL1

ID Q9NZL1 PRELIMINARY; PRT; 396 AA.

AC Q9NZL1;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Aspartyl protease.

GN BACE2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20422477; PubMed=10965118;

RA Solans A., Estivill X., de La Luna S.;

RT "A new aspartyl protease on 21q22.3, BACE2, is highly similar to

RT Alzheimer's amyloid precursor protein beta-secretase.";

RL Cytogenet. Cell Genet. 89:177-184(2000).

CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.

DR EMBL; AF188277; AAF35836.1; -.
 DR HSSP; P00797; 2REN.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 KW Aspartyl protease; Hydrolase; Protease.
 SQ SEQUENCE 396 AA; 43013 MW; 5023A7AF391CEAC9 CRC64;

Query Match 73.2%; Score 1966; DB 4; Length 396;
 Best Local Similarity 100.0%; Pred. No. 4.5e-145;
 Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP	60
Db	1	MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP	60
Qy	61	ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Db	61	ALALEPALASPAGAAFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAG	120
Qy	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTGQSWTGFGVGEDLVTIPKGFNTSFLVNIATI	180
Db	121	TPHSYIDTYFDTERSSTYRSKGFDTVKYTGQSWTGFGVGEDLVTIPKGFNTSFLVNIATI	180
Qy	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Db	181	FESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVA	240
Qy	241	GGTGNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Db	241	GGTGNGGSLVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKA	300
Qy	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Db	301	IVDSGTTLLRLPQKVFDVAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI	360
Qy	361	YLRDENSSRSFRITILPQ	378
Db	361	YLRDENSSRSFRITILPQ	378

RESULT 8

Q7T0Y2

ID Q7T0Y2 PRELIMINARY; PRT; 500 AA.

AC Q7T0Y2;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

QY 133 ERSSTYRSKGFDTVTKYTQGSWTGFGEDLVITPKGFNTSFLVNIATIFESENFFLPGIK 192
 : |::|:| :||:||||||| :|:|:|:|||| | :||:||||:|:|:|:| |
 Db 117 KLSTSYQSLNTEVTVRYTQGSWTGLLGKDVVSIPKGVNGTFLINIASIFQSESFFLPNIN 176

QY 193 WNGILGLAYATLAKPSSSLETFDLSVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLG 252
 | |||||:||||||:| ||||| | ||:||||||| :| | |||||
 Db 177 WQGILGLAYSTLAKPSSSVEPFFDSLVQQENIPDVFSMQMCGAGQSSPGNGINAGSLVLG 236

QY 253 GIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLRLRP 312
 |:||||||:||||| |||||:|:| |:| | |||| | |:|||||||
 Db 237 GVEPSLYKGNWYTPITEEWYYQVEVLKFEVGGQRLNLDCTVYNSDKAIVDSGTTLRLRP 296

QY 313 QKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENSRSRFR 372
 ||:|:|:|: : || | : | | | |||| : : ||:| | |||| | :| ||||
 Db 297 DKVFNAMVDAIVQTSLIQNFNAEFWAGLQACWDKTQPPWNYFPDISIYLRDTNTRSFR 356

QY 373 ITILPQLYIQPMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASP 432
 :|: | |||| : : | :| |||| | : | ||||| ||||| :| |||| |
 Db 357 LTLKPQLYIQSVLTFQESLNCFRFGISQSASTLVIGATVMEGFYVIFDRAEKRVGFAVSS 416

QY 433 CAEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLVLLLL 492
 ||:|:| | ||:| | | ||:|:| | ||:|:|:|:|:| | ||||:| ||||
 Db 417 CAEVSGITVSEIAGPFGTSDVSSNCIARNPLREPIMWIIISYSLMSLCGMILLVLVLLLL 476

QY 493 PFRCQRRPRDPEVVNDESSLVRHRWK 518
 | :| | | :|||||:||||
 Db 477 SNR--QRHDDMETINDESSLVQHRWK 500

RESULT 9

Q9R1P7

ID Q9R1P7 PRELIMINARY; PRT; 255 AA.
 AC Q9R1P7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Aspartyl protease (Fragment).
 GN BACE2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Accarino M., Fumagalli P., Taramelli R., Ottolenghi S.;
 RT "Cloning of a gene from chromosome 21 Down Region encoding a potential
 RT transmembrane protease."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF051150; AAD45964.1; -.
 DR MEROPS; A01.041; -.
 DR MGD; MGI:1860440; Bace2.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR009007; Pept_A_acid.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.

DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 SQ SEQUENCE 501 AA; 55761 MW; B410DA8B64647663 CRC64;

Query Match 44.1%; Score 1186; DB 11; Length 501;
 Best Local Similarity 46.2%; Pred. No. 5.4e-84;
 Matches 238; Conservative 82; Mismatches 169; Indels 26; Gaps 7;

Qy 9 LLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTGPPTPAERHADGLALA 63
 : | | | | : | | | | | | | | | | :
 Db 1 MAPALHWLLLWVGSGMLPAQGTHLGLRLPLRSLA-----GPPLGLRLPRETDEES----- 51

Qy 64 LEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPH 123
 | : | : | | | | : | | : | | | | | | | | | | | | | |
 Db 52 -----EEPGRRGSFVEMVDNLRGKSGQGYVEMTIGSPQTLNILVDTGSSNFAVGAAPH 106

Qy 124 SYIDTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFES 183
 : : | : : | | | | | | | | | | | : | | | : | | | | | |
 Db 107 PFLHRYYQRQLSSTYRDLRGVYPYTQGWEGELGTDLVSIHPGPNVTVRANIAAITES 166

Qy 184 ENFFLPGIKWNGILGLAYATIAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV---A 240
 : | | : | | | | | | | : | | | | | | | | | | : | : | : | : | : | :
 Db 167 DKFFINGSNWEIGLGLAYAEIARPDSSLEPFFDSLQTHIPNIFSLQLCGAGFPLNQTE 226

Qy 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYQIEILKLEIGGQSLNLDCREYNADKA 300
 : | | : : | | : | | : | | : | | : | : | | | | : | : | | | | :
 Db 227 ALASVGGSMIIGGIDHSLYTGSWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYNYDKS 286

Qy 301 IVDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISI 360
 | | | | | | | | | : | | : | : | | : | | | | | | | | : | | | :
 Db 287 IVDSGTTNRLPKKVFEAAVKSIIKAASSTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISL 346

Qy 361 YLRDENSSRSFRITILPQLYIQPMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIF 419
 | | | : : | | | | | | | : : : : : | : | : | : | : | : | : | : | :
 Db 347 YLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVF 406

Qy 420 DRAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVC 479
 | | : | : | | | | | : : | | | | : | | : | : | : | : | : | : | :
 Db 407 DRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAAIC 466

Qy 480 GAILLVLLVLLLLPFRQCR--RPRDPEVVNDESSL 512
 | : : : | : : | | : : : | | |
 Db 467 -ALFMLPLCLMVCQWRCLRLRHQHDDFADDISLL 500

RESULT 11

Q9ULS1

ID Q9ULS1 PRELIMINARY; PRT; 532 AA.

AC Q9ULS1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein KIAA1149 (Fragment).

GN KIAA1149.

OS Homo sapiens (Human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirosawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the GeneMark analysis
RT from size-fractionated cDNA libraries from human brain.";
RL DNA Res. 6:329-336(1999).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.
DR EMBL; AB032975; BAA86463.2; -.
DR HSSP; P56272; 1AM5.
DR GO; GO:0004194; F:pepsin A activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001969; Aspprotease_AS.
DR InterPro; IPR001461; Peptidase_A1.
DR InterPro; IPR009007; Pept_A_acid.
DR Pfam; PF00026; asp; 1.
DR PRINTS; PR00792; PEPSIN.
DR PROSITE; PS00141; ASP_PROTEASE; 1.
KW Hypothetical protein; Aspartyl protease; Hydrolase; Protease.
FT NON_TER 1 1
SQ SEQUENCE 532 AA; 58720 MW; 98B135D0D5FBD2E8 CRC64;

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Qy	44	APTPGPGTPAERHADGLALAL-----EPALASPAGAAANFLAMVDNLQGDSDGRGYYLE	95
Db	52	APSTASGCPCAAAWGGAPLGLRLPRETDEEP--EPPGRRGSFVEMVDNLRGKSGQGYVE	109
Qy	96	MLIGTPPQKLQILVDTGSSNFAVAGTPHSYIDTYFDTERSSTYRSKGFDTVTKYTQGSWT	155
Db	110	MTVGSPPTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSSTYRDLRKGVVPYPTQGKWE	169
Qy	156	GFVGEDLVTPKGFNTSFLVNIATIFESENFLLPGIKWNGILGLAYATLAKPSSSLETFE	215
Db	170	GELGTDLVSIHPGPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDSSLEPFF	229
Qy	216	DSLVTQANIPNVFSMQMCGAGLPVAGS---GTNGGSLVLGGIEPSLYKGDIWYTPIKEEW	272
Db	230	DSLVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREW	289
Qy	273	YYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLRLPQKVFDAAVEAVARASLIPEF	332
Db	290	YYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPLPKKVFEAAVKSIIKAASSTEKF	349
Qy	333	SDGFWTGSQLACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQLYIQPMMGAGLNY-	391
Db	350	PDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRTILPQQYLRFVEDVATSQD	409
Qy	392	ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAIEIAGAAVSEISGPFSTE	451

Db 410 DCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTL 469

Qy 452 DVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLPFRCQR--RPRDPEVVNDE 509
|: | | ::| : ::| |: :: : |: : :|| | | : : :|

Db 470 DMEDCGYNIPQTDESTLMTIAYVMAAIC-ALFMLPLCLMVCQWRCLRCLRQQHDDFADDI 528

Qy 510 SSL 512
| |

Db 529 SLL 531

RESULT 12

Q8BQY4

ID Q8BQY4 PRELIMINARY; PRT; 501 AA.

AC Q8BQY4;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Beta-site APP cleaving enzyme.

GN BACE.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

DR EMBL; AK046175; BAC32620.1; -.

DR MGD; MGI:1346542; Bace.

DR GO; GO:0004194; F:pepsin A activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR001969; Aspprotease_AS.

DR InterPro; IPR001461; Peptidase_A1.

DR InterPro; IPR009007; Pept_A_acid.

DR Pfam; PF00026; asp; 1.

DR PRINTS; PR00792; PEPSIN.

DR PROSITE; PS00141; ASP_PROTEASE; 1.

SQ SEQUENCE 501 AA; 55816 MW; C0855513145E024E CRC64;

Query Match 44.0%; Score 1183; DB 11; Length 501;

Best Local Similarity 46.0%; Pred. No. 9.2e-84;

Matches 237; Conservative 83; Mismatches 169; Indels 26; Gaps 7;

Qy 9 LLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTGPGPPTAERHADGLALA 63
: | | | | : | | | | | | | | | | : |

Db 1 MAPALHWLLWVGSGMLPAQGTHLGIRLPLRSGLA-----GPPLGLRLPRETDEES----- 51

Qy 64 LEPALASPAGAANFLAMVDNLQGDSDRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPH 123
| :|: | | | | :| | | | | :|: | | | | | | | | | | | |

Db 52 -----EEPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPFQTLNILVDTGSSNFAVGAAPH 106

QY 124 SYIDTYFDTERSSTYRSKGFVDVTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFES 183
 :: | : : |||| | | |||| | : | ||:| | | : || | ||
 Db 107 PFLHRYYQRLSSTYRDLRGVYVPYTQGWEGELGTDLVSI PHGPNVTVRANIAAITES 166

QY 184 ENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV---A 240
 : ||: | | ||||| :|: | || |||| | :||:|:|:|:| | :
 Db 167 DKFFINGSNWEGILGLAYAEIARPDSDLPEFFDSLVKQTHIPNIFSLQLCGAGFPLNQTE 226

QY 241 GSGTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKA 300
 : |||::|:| | | :|||: |||: |::| | | :|:| | | :
 Db 227 ALASVGGSMIIGGIDHSLYTGR LWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKS 286

QY 301 IVDSGTTLLRLPQKVFDVAVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISI 360
 ||||| |||:|:| | ::: | | : | || | | | | ||: | | | :
 Db 287 IVDSGTTNRLPKKVFEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISL 346

QY 361 YLRDENSSRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIF 419
 || | ::||| || | :|: : : ||:| : | : | :| :||| | :
 Db 347 YLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVF 406

QY 420 DRAQKRVGFAASPCAIEIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVC 479
 |||:|:| | | : : || | | : | | :| : : :
 Db 407 DRARKRIGFAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAAIC 466

QY 480 GAILLVLLIVLLLLPFRQR--RPRDPEVVNDESSL 512
 | : : : | : : || | | : : : | | |
 Db 467 -ALFMLPLCLMVCQWRCLRLRHQHDDFADDISLL 500

RESULT 13

Q8IYC8

ID Q8IYC8 PRELIMINARY; PRT; 501 AA.
 AC Q8IYC8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-site APP-cleaving enzyme.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC036084; AAH36084.1; -.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001969; Aspprotease_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 DR PRINTS; PR00792; PEPSIN.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 SQ SEQUENCE 501 AA; 55824 MW; 768595CF5517EFB7 CRC64;

Query Match 43.6%; Score 1172.5; DB 4; Length 501;
 Best Local Similarity 46.1%; Pred. No. 6.1e-83;
 Matches 239; Conservative 82; Mismatches 165; Indels 33; Gaps 9;

```

QY      7 ALLLPLLAQWLLRAAPELAPAPFT-----LPLRVAAATNRVVAPTPGPGTPAERHADGLA 61
      |  |  |  | :      :  |  |      |  |  |  |  |  |  |  |
Db      2 AQALPWLLLWM---GAGVLPAGHTQHGI RLPLRSLGLG-----GAPL-----GLR 42

QY     62 LALE--PALASPAGAAANFLAMVDNLQGDSDGRGYYLEMLIGTPPQKLQILVDTGSSNFAVA 119
      |  |      |      :|: |||||:| ||:||||:| |:||| | |||||
Db     43 LPRETDEEPEEPGRRGSFVEMVDNLRGKSGQGYVEMTVGSPQTINILVDTGSSNFAVG 102

QY    120 GTPHSYIDTYFDTERSSTYRSKGFVDVTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIAT 179
      || :: | : : |||| | | |||| | | :| |||:| | | : |||
Db    103 AAPHPFLHRYYQRQLFSTYRDLRKGVVYPYTQGWEGELGTDLSIPHGNVTVRANIAA 162

QY    180 IFESENFFLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPV 239
      | ||: ||: | | ||||| ||:| ||| ||||| | :||: ||:| ||| | :
Db    163 ITESDKFFINGSNWEGILGLAYAEIARPDSSLEPFFDSLVKQTHVPLNLSQLCGAGFPL 222

QY    240 AGS---GTNGGSLVLGGIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYN 296
      | : |||::|||: || | :|||: |||: : |:| | | | :||: |||
Db    223 NQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYN 282

QY    297 ADKAIVDSGTTLRLRPQKVFDVAVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFP 356
      ||:||||| |||: |||: |::: || :| ||| | || || |||: ||
Db    283 YDKSIVDSGTTLRLRPKKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFP 342

QY    357 KISIIYLRDENSRSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGF 415
      ||: || | ::||| |||| |::| : : ||: | || | : | : |||
Db    343 VISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF 402

QY    416 YVIFDRAQKRVGFAASPCAETAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYAL 475
      ||:||||: ||: || | | : : ||| | | : | | | : | :
Db    403 YVVFDRAKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDESTLMTIAYVM 462

QY    476 MSVCGAILLVLLIVLLLLPFRQR--RPRDPEVVNDESSL 512
      ::| | : : : |:: :|| | | : : : | | |
Db    463 AAIC-ALFMLPLCLMVCQWRCLRCLRQHQHDDFADDISLL 500

```

RESULT 14

Q8C4F4

ID Q8C4F4 PRELIMINARY; PRT; 467 AA.

AC Q8C4F4;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Beta-site APP cleaving enzyme.

GN BACE.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RESULT 15

Q9CUU5

ID Q9CUU5 PRELIMINARY; PRT; 267 AA.
AC Q9CUU5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adult male brain cDNA, RIKEN full-length enriched library,
DE clone:3526402A15 product:beta-site APP cleaving enzyme, full insert
DE sequence (Fragment).
GN BACE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [5]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 DR EMBL; AK014390; BAB29317.2; -.
 DR MGD; MGI:1346542; Bace.
 DR GO; GO:0004194; F:pepsin A activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009007; Pept_A_acid.
 DR Pfam; PF00026; asp; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 267 AA; 30333 MW; 9413EB4530AB63B0 CRC64;

Query Match 24.3%; Score 653; DB 11; Length 267;
 Best Local Similarity 45.3%; Pred. No. 8.8e-43;
 Matches 121; Conservative 56; Mismatches 86; Indels 4; Gaps 3;

QY 249 LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVDSGTTL 308
 :::|||: ||| :|||: |||: |::|| || :||: ||| ||: |||||
 Db 1 MIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTN 60
 QY 309 LRLPQKVFD AVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISYLRDENSS 368
 |||: |||: | ::: || :| ||| | || || ||: || ||: || | ::
 Db 61 LRLPKKVFEAAVKSIAASSTEKFPDGEWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTN 120
 QY 369 RSFRITILPQLYIQPMMGAGLNY-ECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVG 427
 :||| ||||| |::: : :||: | :| :| :|| :||| |||: |||: |
 Db 121 QSFRITILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIMEGFYVVFDRARKRIG 180
 QY 428 FAASPCAETIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLI 487
 || | | : : ||| | : | | :| : :| :| : : :
 Db 181 FAVSACHVHDEFRTAAVEGPFVTADMEDCGYNIPQTDESTLMTIAYVMAAIC-ALEMLPL 239
 QY 488 VLLLLLPFRCQR--RPRDPEVVNDESSL 512
 |:: :|| | | : : :| ||
 Db 240 CLMVCQWRCLRLRHQHDDFADDISLL 266

Search completed: February 28, 2004, 09:11:16

Job time : 45.4848 secs